

Annex 1

**PBP2X AMINO ACID SEQUENCE ACCESSION NUMBERS
AVAILABLE IN THE SEQUENCE DATA BASES
AT THE PRIORITY DATE (11 JULY 2002)**

1PMD
P14677
AAC45547
AAC95456
AAD45394
AAF17263
AAF17264
AAF17265
AAF17266
AAF17267
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AAF17269
AAF17270
AAL77081
AAL82396
AAL82397
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BAA75534
BAA75535
BAA75536
BAA75537

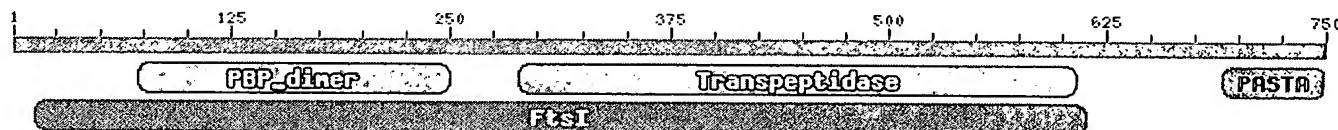
BAA75538
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CAA46263
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CAA46265
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CAA67013
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CAC20947
CAC20948
CAC20949
CAC20950
CAC20951
CAC20952
CAC20953
CAC20954
CAC20955
CAC43044
CAC43045

BLAST Basic Local Alignment Search Tool

Job Title: PBP2X-R6

Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.



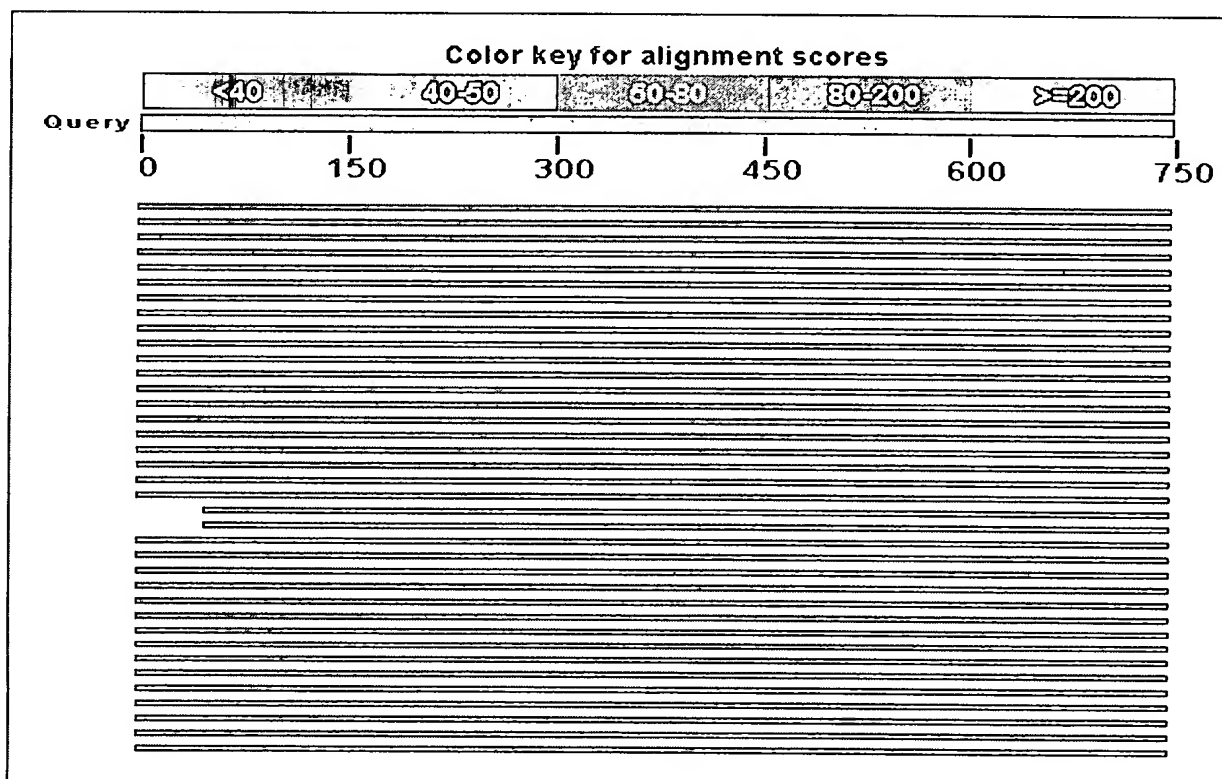
- Your search is limited to records matching entrez query: PBP2x penicillin binding protein AND Streptococcus pneumoniae [ORGN].

BLASTP 2.2.16 (Mar-25-2007)

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference: Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005. RID: 5ZZGCTZA015 **Database:** All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects 4,990,428 sequences; 1,725,524,515 total letters

Query= Length=750

Distribution of 100 Blast Hits on the Query Sequence


Distance tree of results ^{NEW} Related Structures

Sequences producing significant alignments:

	Score (Bits)	E Value	
sp P59676 PBPX_STRR6 Penicillin-binding protein 2X (PBP-2X) (PBP	1441	0.0	G
dbj BAD00902.1 penicillin-binding protein 2X [Streptococcus pne	1439	0.0	
dbj BAD67448.1 penicillin-binding protein 2X [Streptococcus pne	1438	0.0	
sp P14677 PBPX_STRPN Penicillin-binding protein 2x (PBP-2x) (PBP	1438	0.0	
dbj BAD00901.1 penicillin-binding protein 2X [Streptococcus pne	1438	0.0	
dbj BAD00904.1 penicillin-binding protein 2X [Streptococcus pne	1436	0.0	
gb AAF17263.1 AF210753_1 penicillin-binding protein 2X [Streptoc	1434	0.0	
dbj BAD00905.1 penicillin-binding protein 2X [Streptococcus ...	1418	0.0	
dbj BAD00912.1 penicillin-binding protein 2X [Streptococcus pne	1415	0.0	
gb AAF17266.1 AF210756_1 penicillin-binding protein 2X [Streptoc	1397	0.0	
gb AAF17265.1 AF210755_1 penicillin-binding protein 2X [Strep...	1395	0.0	
dbj BAD00920.1 penicillin-binding protein 2X [Streptococcus pne	1368	0.0	
dbj BAD00903.1 penicillin-binding protein 2X [Streptococcus pne	1367	0.0	
dbj BAD00916.1 penicillin-binding protein 2X [Streptococcus pne	1365	0.0	
gb AAF17267.1 AF210757_1 penicillin-binding protein 2X [Streptoc	1361	0.0	
dbj BAD00919.1 penicillin-binding protein 2X [Streptococcus pne	1357	0.0	
gb AAF17264.1 AF210754_1 penicillin-binding protein 2X [Streptoc	1349	0.0	
dbj BAD00929.1 penicillin-binding protein 2X [Streptococcus pne	1348	0.0	
dbj BAD00909.1 penicillin-binding protein 2X [Streptococcus pne	1345	0.0	
dbj BAD00907.1 penicillin-binding protein 2X [Streptococcus pne	1344	0.0	
pdb 1QME A Chain A, Penicillin-Binding Protein 2x (Pbp-2x) >p...	1344	0.0	S
pdb 1PYY A Chain A, Double Mutant Pbp2x T338aM339F FROM STREP...	1341	0.0	S
dbj BAD00918.1 penicillin-binding protein 2X [Streptococcus pne	1340	0.0	
dbj BAD00910.1 penicillin-binding protein 2X [Streptococcus pne	1336	0.0	
dbj BAD00923.1 penicillin-binding protein 2X [Streptococcus ...	1327	0.0	
dbj BAD00917.1 penicillin-binding protein 2X [Streptococcus pne	1324	0.0	
dbj BAD00927.1 penicillin-binding protein 2X [Streptococcus pne	1323	0.0	
dbj BAD00913.1 penicillin-binding protein 2X [Streptococcus pne	1318	0.0	
dbj BAD00938.1 penicillin-binding protein 2X [Streptococcus pne	1316	0.0	
dbj BAD00922.1 penicillin-binding protein 2X [Streptococcus pne	1316	0.0	
dbj BAD00925.1 penicillin-binding protein 2X [Streptococcus pne	1315	0.0	
dbj BAD00926.1 penicillin-binding protein 2X [Streptococcus pne	1315	0.0	
gb AAF17268.1 AF210758_1 penicillin-binding protein 2X [Streptoc	1313	0.0	
gb AAF17270.1 AF210760_1 penicillin-binding protein 2X [Streptoc	1312	0.0	
dbj BAD00932.1 penicillin-binding protein 2X [Streptococcus pne	1312	0.0	
gb AAF17269.1 AF210759_1 penicillin-binding protein 2X [Streptoc	1312	0.0	
dbj BAD00936.1 penicillin-binding protein 2X [Streptococcus pne	1312	0.0	
gb AAL77081.1 AF468152_1 penicillin-binding protein 2X [Streptoc	1307	0.0	
dbj BAD00939.1 penicillin-binding protein 2X [Streptococcus pne	1307	0.0	
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dbj BAD00906.1 penicillin-binding protein 2X [Streptococcus pne	1305	0.0	
dbj BAD00937.1 penicillin-binding protein 2X [Streptococcus pne	1303	0.0	
pdb 1RP5 A Chain A, Pbp2x From Streptococcus Pneumoniae Strai...	1297	0.0	S
dbj BAD00914.1 penicillin-binding protein 2X [Streptococcus ...	1296	0.0	
dbj BAD00928.1 penicillin-binding protein 2X [Streptococcus pne	1294	0.0	
pdb 1PMD Chain , Penicillin-Binding Protein 2x (Pbp-2x)	1294	0.0	S
gb AAC45547.1 low-affinity penicillin-binding protein 2X [St...	1284	0.0	
dbj BAD00915.1 penicillin-binding protein 2X [Streptococcus pne	1279	0.0	
dbj BAD00940.1 penicillin-binding protein 2X [Streptococcus pne	1275	0.0	
gb AAY56845.1 penicillin-binding protein 2X [Streptococcus pneu	1271	0.0	
dbj BAD00908.1 penicillin-binding protein 2X [Streptococcus ...	1269	0.0	
gb ABB46504.1 penicillin binding protein 2x [Streptococcus p...	1258	0.0	
gb AAN32862.1 penicillin-binding protein 2X [Streptococcus pneu	1235	0.0	
gb AAN32857.1 penicillin-binding protein 2X [Streptococcus p...	1234	0.0	
emb CAB65447.1 penicillin binding protein 2x [Streptococcus pne	1230	0.0	
gb AAN32865.1 penicillin-binding protein 2X [Streptococcus pneu	1222	0.0	
emb CAD90770.1 penicillin-binding protein 2x [Streptococcus pne	1217	0.0	
emb CAD90771.2 penicillin-binding protein 2x [Streptococcus pne	1209	0.0	
gb AAY56843.1 penicillin-binding protein 2X [Streptococcus p...	1207	0.0	
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gb AAY56847.1 penicillin-binding protein 2X [Streptococcus pneu	1204	0.0	

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gb AA56857.1	penicillin-binding protein 2X [Streptococcus pneu	1197	0.0
emb CAB65444.1	penicillin binding protein 2x [Streptococcus pne	1188	0.0
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pdb 1K25 A	Chain A, Pbp2x From A Highly Penicillin-Resistant ...	1183	0.0
gb ABB46505.1	penicillin binding protein 2x [Streptococcus pneu	1182	0.0
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gb AA56848.1	penicillin-binding protein 2X [Streptococcus pneu	1180	0.0
emb CAB65446.1	penicillin binding protein 2x [Streptococcus pne	1179	0.0
gb AAN32859.1	penicillin-binding protein 2X [Streptococcus pneu	1176	0.0
gb AA56854.1	penicillin-binding protein 2X [Streptococcus pneu	1174	0.0
gb AAN32860.1	penicillin-binding protein 2X [Streptococcus pneu	1174	0.0
gb AA56839.1	penicillin-binding protein 2X [Streptococcus pneu	1170	0.0
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gb AA56852.1	penicillin-binding protein 2X [Streptococcus pneu	1158	0.0
emb CAB65441.1	penicillin binding protein 2x [Streptococcus pne	1157	0.0
gb AAN32855.1	penicillin-binding protein 2X [Streptococcus pneu	1157	0.0
gb AA56849.1	penicillin-binding protein 2X [Streptococcus pneu	1155	0.0
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gb AA56841.1	penicillin-binding protein 2X [Streptococcus pneu	1150	0.0
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emb CAA88919.1	penicillin-binding protein 2x [Streptococcus pne	1149	0.0
emb CAB65448.1	penicillin binding protein 2x [Streptococcus pne	1148	0.0
emb CAA67012.1	penicillin-binding protein [Streptococcus pneumo	1148	0.0
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gb AA56856.1	penicillin-binding protein 2X [Streptococcus pneu	1145	0.0
gb AAN32864.1	penicillin-binding protein 2X [Streptococcus pneu	1143	0.0
emb CAA67011.1	penicillin-binding protein [Streptococcus pneumo	1141	0.0
gb AA56840.1	penicillin-binding protein 2X [Streptococcus pneu	1140	0.0
gb AAN32856.1	penicillin-binding protein 2X [Streptococcus pneu	1139	0.0
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gb AA56855.1	penicillin-binding protein 2X [Streptococcus pneu	1135	0.0

Alignments

>sp|P59676|PBPX_STRR6  Penicillin-binding protein 2X (PBP-2X) (PBP2X)
Length=750

Score = 1441 bits (3729), Expect = 0.0, Method: Composition-based stats.
Identities = 750/750 (100%), Positives = 750/750 (100%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHXYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHXYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYPGSTMKVMMLAAAI DNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYPGSTMKVMMLAAAI DNNTFPGGEVFN	360

Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGRMMTFSSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDVPYGTMYNHSTGKPTVTV	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDVPYGTMYNHSTGKPTVTV	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLIILSDKAEVDPMYGWTKETATLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIKNSSAEEGKNLAPNQVLIILSDKAEVDPMYGWTKETATLAKWLNIELEF	720
Query	721	QSGGSTVQKQDVRANTAIKDIKKITLTLGD	750
Sbjct	721	QSGGSTVQKQDVRANTAIKDIKKITLTLGD	750

>dbj|BAD00902.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1439 bits (3726), Expect = 0.0, Method: Composition-based stats.
Identities = 749/750 (99%), Positives = 749/750 (99%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPFTFADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGEVFN	360
Sbjct	301	ILATTQRPFTFADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGRMMTFSSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDVPYGTMYNHSTGKPTVTV	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDVPYGTMYNHSTGKPTVTV	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLIILSDKAEVDPMYGWTKETATLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIKNSSAEEGKNLAPNQVLIILSDKAEVDPMYGWTKETATLAKWLNIELEF	720
Query	721	QSGGSTVQKQDVRANTAIKDIKKITLTLGD	750
Sbjct	721	QSGGSTVQKQDVRANTAIKDIKKITLTLGD	750

Sbjct 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

>dbj|BAD67448.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1438 bits (3723), Expect = 0.0, Method: Composition-based stats.
Identities = 748/750 (99%), Positives = 748/750 (99%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGVEFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGVEFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLILSDKAEVDPDYGWTKETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIKNSSAEEGKNLAPNQVLILSDKAEVDPDYGWTKETAETLAKWLNIELEF	720
Query	721	QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750	

>sp|P14677|PBPX_STRPN Penicillin-binding protein 2x (PBP-2x) (PBP2x)
Length=750

Score = 1438 bits (3723), Expect = 0.0, Method: Composition-based stats.
Identities = 749/750 (99%), Positives = 749/750 (99%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300

Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGRMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSCKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVSCKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLILSDKAEVDPMYGWTKETATLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIKNSSAEEGKNLAPNQVLILSDKAEVDPMYGWTKETATLAKWLNIELEF	720
Query	721	QSGGSTVQKQDVRANTAIKDIKKITLTLGD	750
Sbjct	721	QSGGSTVQKQDVRANTAIKDIKKITLTLGD	750

>dbj|BAD00901.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1438 bits (3722), Expect = 0.0, Method: Composition-based stats.
Identities = 748/750 (99%), Positives = 749/750 (99%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLQVVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLQVVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSCKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVSCKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLILSDKAEVDPMYGWTKETATLAKWLNIELEF	720

```

_Sbjct 661  IVVGTGTRVIRYATKNRSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 720
              IVVGTGTRVIRYATKNRSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK
Query 721  QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
              QGSGSTVQKQDVRANTAIKDIKKITLTLGD
_Sbjct 721  QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

```

>dbj|BAD00904.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1436 bits (3718), Expect = 0.0, Method: Composition-based stats.
Identities = 748/750 (99%), Positives = 749/750 (99%), Gaps = 0/750 (0%)

```

Query 1      MKWTKRVIRYATKNRSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1      MKWTKRVIRYATKNRSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

Query 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

Query 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF 180

Query 181    TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181    TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240

Query 241    LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE 300
Sbjct 241    LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE 300

Query 301    ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGEVFN 360
Sbjct 301    ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGEVFN 360

Query 361    SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGGDATWLDYLNRFK 420
Sbjct 361    SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGGDATWLDYLNRFK 420

Query 421    FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421    FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480

Query 481    SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481    SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540

Query 541    GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541    GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600

Query 601    GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601    EEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660

Query 661    IVVGTGTRVIRYATKNRSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 720
Sbjct 661    IVVGTGTRVIRYATKNRSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 720

Query 721    QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721    QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

```

>gb|AAF17263.1|AF210753_1 penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1434 bits (3713), Expect = 0.0, Method: Composition-based stats.
Identities = 747/750 (99%), Positives = 748/750 (99%), Gaps = 0/750 (0%)

```

Query 1      MKWTKRVIRYATKNRSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1      MKWTKRVIRYATKNRSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

Query 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

Query 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF 180

Query 181    TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240

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Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE	300
Sbjct	241	LGNIIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSFDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVSFDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLISDKAEVDPMYGWTKETATLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLISDKAEVDPMYGWTKETATLAKWLNIELEF	720
Query	721	QSGGSTVQKQDVRANTAIKDIKKITLTLGD	750
Sbjct	721	QSGGSTVQKQDVRANTAIKDIKKITLTLGD	750

>dbj|BAD00905.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 dbj|BAD00921.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 Length=750

Score = 1418 bits (3670), Expect = 0.0, Method: Composition-based stats.
 Identities = 737/750 (98%), Positives = 745/750 (99%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTRTTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTRTTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE	300
Sbjct	241	LGNIIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGLTKDFVWRDILYQSNYEPGSTMKVMTLAAIDNNTFPGGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSFDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SALYDPNDQSVRKSQKEIVGNPVSFDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600

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Query 601  GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601  GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660

Query 661  IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVDPMYGWTKETAE TLAKWLNIELEF 720
Sbjct 661  IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVDPMYGWTKETAE TLAKWLNIELEF 720

Query 721  QGSGSTVQKQDV RANTAIKDIKKITLTLGD 750
Sbjct 721  QGSGSTVQKQDV RANTAIKDIKKITLTLGD 750

```

>dbj|BAD00912.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1415 bits (3662), Expect = 0.0, Method: Composition-based stats.
Identities = 734/750 (97%), Positives = 744/750 (99%), Gaps = 0/750 (0%)

```

Query 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

Query 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

Query 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KGNGITYANMMSIKKELEAEVKGIDF 180

Query 181    TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181    TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNILAGTDGIITYEKDR 240

Query 241    LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMATLVSAKTGE 300
Sbjct 241    LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMATLVSAKTGE 300

Query 301    ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGEVFN 360
Sbjct 301    ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGEVFN 360

Query 361    SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361    SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420

Query 421    FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421    FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480

Query 481    SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481    SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540

Query 541    GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541    GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600

Query 601    GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601    GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660

Query 661    IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVDPMYGWTKETAE TLAKWLNIELEF 720
Sbjct 661    IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVDPMYGWTKETAE TLAKWLNIELEF 720

Query 721    QGSGSTVQKQDV RANTAIKDIKKITLTLGD 750
Sbjct 721    QGSGSTVQKQDV RANTAIKDIKKITLTLGD 750

```

>gb|AAF17266.1|AF210756_1 penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1397 bits (3617), Expect = 0.0, Method: Composition-based stats.
Identities = 725/750 (96%), Positives = 737/750 (98%), Gaps = 0/750 (0%)

```

Query 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

Query 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61     EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

```

Query	121	KVAEVFHXYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHXYLDMEESYV EQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKYMATLVS AKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKYMATLVS AKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFP GG EVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFP GE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIA S+FGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNM+LVGTD PVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVALKSGTA+IADEKNGGYLVG T+ IFS V+M+PAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFTNPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQOVLILSDKAEVVPD MYGWT KETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIKNSSAEEGKNLAPNQOVLILSDKAEVVPD MYGWT TAET AKWLNIELEF	720
Query	721	QGS GSTVQKQDVRANTAIKD IKKITLTLGD 750	
Sbjct	721	EGSGSTVQKQDVRANTAIKD IKKITLTLGD 750	

>gb|AAF17265.1|AF210755 1 penicillin-binding protein 2X [Streptococcus pneumoniae]
 gb|AAC95456.1| penicillin-binding protein 2x [Streptococcus pneumoniae]
 Length=750

Score = 1395 bits (3612), Expect = 0.0, Method: Composition-based stats.
 Identities = 723/750 (96%), Positives = 737/750 (98%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHXYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHXYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKYMATLVS AKTGE	300
Sbjct	241	LGNIVPGTEQVSQQTVDGKDVYTTISSPLQSFMETQMDAFQEKVKGKYMATLVS AKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFP GG EVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFP GG EVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIA S+FGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540

```

_Sbjct  481  SA+YDPNDQ+ RKSQKEIVGNPVSK+AAS+TR +MV+VGTD P YGTMYNHSTGK TV VP
          SALYDPNDQSVRKSQKEIVGNPVSKAASVTRDHMMVVGTDPTYGTMYNHSTGKATVNV P 540
Query    541  GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
          GQNVALKSGTA+IADEKNGGYL G T+ IFS VSM PAENPDFILYVTVQQPEHYSGIQL
_Sbjct  541  GQNVALKSGTAQIADEKNGGYLTGSTNNIFSVVSMHPAENPDFILYVTVQQPEHYSGIQL 600
Query    601  GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
          GEFANPILERASAMK+SLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP
Sbjct    601  GEFANPILERASAMKESLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Query    661  IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPDYGWTKETAETLAKWLNIELEF 720
          IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPDYGWTKETAET AKWLNIELEF
Sbjct    661  IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPDYGWTKETAETFAKWLNIELEF 720
Query    721  QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
          +GSGSTVQKQDVRANTAIKDIKKITLTLGD
Sbjct    721  EGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

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>dbj|BAD00920.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1368 bits (3540), Expect = 0.0, Method: Composition-based stats.
Identities = 708/750 (94%), Positives = 731/750 (97%), Gaps = 0/750 (0%)

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Query    1  MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
          MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVIIGTGTRFGTDLAK
Sbjct    1  MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAVFLVNFAVIIGTGTRFGTDLAK 60
Query    61  EAKKVHQTTTRTPAKRGTIYDRNGVPVIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
          EAKKVHQTTTRTPAKRGTIYDRNGVPVIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN
Sbjct    61  EAKKVHQTTTRTPAKRGTIYDRNGVPVIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Query    121  KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
          KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KGNGITYANMMSIKKELE AEVKGIDF
Sbjct    121  KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGSKGNGITYANMMSIKKELETAEVKGIDF 180
Query    181  TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
          TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR
Sbjct    181  TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Query    241  LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
          LGNIVPGTEQVSQ+T+DGKDVYTTISS LQSFMETQ+AFQEKVKGYMTATLVSAKTGE
Sbjct    241  LGNIVPGTEQVSQQTVDGKDVYTTISSTLQSFMETQMNAFQEKVKGYMTATLVSAKTGE 300
Query    301  ILATTQRPFTFADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGVEFN 360
          ILATTQRPFTFADTKEG+T+DFVWRDILYQSNYEPGSTMKVM LAA+IDNNTFPGGE FN
Sbjct    301  ILATTQRPFTFADTKEGLTKDFVWRDILYQSNYEPGSTMKVMTLAASIDNNTFPGGVEFN 360
Query    361  SSELKIADATIRDWDVNEGLTGGRMMTFSGQFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
          SSELKIAD TIRDWDVN+GLT GRMMTF QGFA SSNVGM+LLEQKMGDATWLDYLNRFK
Sbjct    361  SSELKIADVTIRDWDVNDGLTTGRMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLNRFK 420
Query    421  FGVPTREFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
          FGVPTREFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI
Sbjct    421  FGVPTREFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480
Query    481  SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDVPYGTMYNHSTGKPTVTV P 540
          SAIYD N+Q+ RKSQKEIVG PVS+DAASLRTNM+LVGTD P+YGTMYNH TGKP +TV P
Sbjct    481  SAIYDTNNQSVRKSQKEIVGKPVSEDAASLRTNMILVGTDPLYGTMYNHQTGKPIITVP 540
Query    541  GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
          GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYS QL
Sbjct    541  GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNP AENPDFILYVTVQQPEHYSAAQL 600
Query    601  GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
          GEF+NPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP
Sbjct    601  GEFNPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Query    661  IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPDYGWTKETAETLAKWLNIELEF 720
          IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPDYGWTK TAET AKWLNIELEF
Sbjct    661  IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPDYGWTKATAETFAKWLNIELEF 720
Query    721  QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
          +GSGSTVQKQDVRANTAIKDIKKITLTLGD
Sbjct    721  EGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

```

>dbj|BAD00903.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1367 bits (3538), Expect = 0.0, Method: Composition-based stats.
Identities = 705/750 (94%), Positives = 727/750 (96%), Gaps = 0/750 (0%)

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Query    1  MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

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Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVN+GLT G MMTFSQGFAHSSNVGM+LLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYTGQLPADNIVNIAMSAFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKS+KEIVG PVS+DAASLTRTNM+LVGTDP+YGTMYNH TGKP +TVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVAKSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERA AMKDSLNLQ+TAK L+QV+ QS Y MPS+KDISPGDLAE LRRN+VQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAEVDPMYGWTKETATLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIK SS EEG NL PNQQVLILSDKAEVDPMYGWTK TAET AKWLN+LEF	720
Query	721	QSGGSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	+GSGGSTVQKQDVRANTAIKDIKKITLTLGD 750	

>dbj|BAD00916.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1365 bits (3534), Expect = 0.0, Method: Composition-based stats.
Identities = 706/750 (94%), Positives = 729/750 (97%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFPGGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGLTKDFVWRDILYQSNYEPGSTMKVMTLASSIDNNTFPSGEYFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIAD TIRDWDVN+GLT GRMMTF QGFA SSVNGM+LLEQKMGD TWLDYLNRFK	420

```

Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI 480

Query 481 SAIYDPNDQTARKSQKEIVGNPNVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYD N+Q+ RKSQKEIVG PVS+DAASLTRTNM+LVGTDP+YGTMYNH TGKP +TVP 540
SAIYDTNNQSVRKSQKEIVGKPVSEDAASLTRTNMILVGTDPYGTMYNHYTGPPIITVP

Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL 600
GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPANPDFILYVTVQQPEHYSGIQL

Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEFANPILERASAMK+SLNLQ+ AK L+QV+ +S Y MPS+KDISPGDLAEELRRNLVQP 660
GEFANPILERASAMKESLNLQSPAKNLDQVTTESYAMPSIKDISPGDLAEELRRNLVQP

Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVPMYGTWKETAETLAKWLNIELEF 720
Sbjct 661 IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDK EEVPMYGTWKETAETLAKWLNIELEF 720
IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKVEEVPDYGWTKETAETLAKWLNIELEF

Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
QGSGSTVQKQDVRANTAIKDIKKITLTLGD

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>gb|AAF17267.1|AF210757_1 penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1361 bits (3522), Expect = 0.0, Method: Composition-based stats.
Identities = 705/750 (94%), Positives = 726/750 (96%), Gaps = 0/750 (0%)

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Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFA+FLVNFAVIIGTGTRFGTDLAK 60
MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFAVFLVNFAVIIGTGTRFGTDLAK

Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQTTTR VPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
EAKKVHQTTTRIVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGGITYANMMSIKKELE AEVKGIDF 180
KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGGITYANMMSIKKELETAEVKGIDF

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR 240
TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR

Query 241 LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQ+T+DGKDVYTTISS LQSFMETQMDAF EKVKGKYMTATLVSAKTGE 300
LGNIVPGTEQVSQQTVDGKDVYTTISS TLQSFMETQMDAFLEKVKGKYMTATLVSAKTGE

Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN 360
Sbjct 301 ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN 360
ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFN

Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK 420
SSEFKIADATTRDWDVNDGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRFK

Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI 480
FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI

Query 481 SAIYDPNDQTARKSQKEIVGNPNVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYD N+Q+ RKSQKEIVGNPNVSK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP 540
SAIYDTNNQSVRKSQKEIVGNPNVSKAASSTRNHMILVGTDPYGTMYNHYTGPPIITVP

Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL 600
GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPANPDFILYVTVQQPEHYSGIQL

Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEFA PILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
GEFATPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP

Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVPMYGTWKETAETLAKWLNIELEF 720
Sbjct 661 IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDK EEVPMYGTWKETAETLAKWLNIELEF 720
IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKVEEVPDYGWTKETAETLAKWLNIELEF

Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
QGSGSTVQKQDVRANTAIKDIKKITLTLGD

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>dbj|BAD00919.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1357 bits (3511), Expect = 0.0, Method: Composition-based stats.
Identities = 699/750 (93%), Positives = 726/750 (96%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTK+VIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELETAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQV Q+T+DGKDVYTTISS LQSFMETQM+AFQEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEG+T+DFVWRDILYQSNYEPGSTMKVM LAAIDNNTFPGGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIAD TIRDWDVNEGLTGGRMMTFSQGF SSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKEAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYDPNDQ+ RKSQKEIVGNPVSKEAAS+TR MV+VGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGLT+YIFSAVSM+PAENPDFILYVTVQQPEHYSIGL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERA AMKDSLNLQ+TAKAL+Q+S Q+ Y MPS+KDISPGDLAEELRRN+VQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVPMYGTWKETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PDMYGW KETAET AKWL+IELEF	720
Query	721	QGS GSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLGD 750	

>gb|AA17264.1|AF210754_1 penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1349 bits (3492), Expect = 0.0, Method: Composition-based stats.
Identities = 696/750 (92%), Positives = 725/750 (96%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTK+VIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KNGNGITYANMM+IKKELEAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQ+T+DGKDVYTTISS LQSFMETQM+AFQEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEG+T+DFVWRDILYQSNYEPGSTMKVM LAAIDNNTFPGGEVFN	360

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-Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSELK+ADATIRDWDVNEGLTGG MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
SSELKVADATIRDWDVNEGLTGGGMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420

-Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FG+PTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
FGIPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480

Query 481 SAIYDPNDQTARKSQKEIVGNPNVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 +A+YDPN+Q+ RKSQKEIVGNPNVSKDAAS TRT+MVLVGTDP YGTMYNHSTGK TV VP 540
TALYDPNNQSVRKSQKEIVGNPNVSKDAASQTRTHMVLVGTDPVYGTMYNHSTGKATVNV 540

Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNVALKSGTA+IADEKNGGYLVG T++IFS V+M+PAENPDFILYVTVQQPEHYSGIQL 600
GQNVALKSGTAEIADEKNGGYLVGSTNHI FSVVAMNPAENPDFILYVTVQQPEHYSGIQL 600

Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEFANPILERA AMKDSLNLQ+TAK L+QV+ QS Y MPS+KDISPGDLAE LRRN+VQP 660
GEFANPILERAVAMKDSLNLQSTAKTLDQVTNQSAYAMPSIKDISPGDLAEALRRNIVQP 660

Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVLLISDKAEVDPMYGWTKEAETLAKWLNIELEF 720
Sbjct 661 IVVGTGTKIK SS EEG NLAPNQVLL+LSDKAEVDPMYGWT KAE +KWLNIEL F 720
IVVGTGTKIKESSVEEGSNLAPNQVLLLSDKAEVDPMYGWT KATAEAFSKWLNIELVF 720

Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721 +GSGSTVQKQDVRANTAIKDIKKITLTLGD 750
EGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

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>dbj|BAD00929.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1348 bits (3489), Expect = 0.0, Method: Composition-based stats.
Identities = 695/750 (92%), Positives = 724/750 (96%), Gaps = 0/750 (0%)

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Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTK+VIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVIIGTGTRFGTDLAK 60
MKWTKKVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAVFLVNFAVIIGTGTRFGTDLAK 60

Query 61 EAKKVHQTTRTVPKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQTTRTVPKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
EAKKVHQTTRTVPKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KNGITYANMMSIKKELE AEVKGIDF 180
KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGSKNGITYANMMSIKKELETAEVKGIDF 180

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR 240
TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGKDGIIITYEKDR 240

Query 241 LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQ+T+DGKDVYTTISS LQSFMETQ+AFQEKVKGYMTATLVSAKTGE 300
LGNIVPGTEQVSQQTVVDGKDVYTTISS TLQSFMETQMNAFQEKVKGYMTATLVSAKTGE 300

Query 301 ILATTQRPFTFADTKEGITEDFVWRDILYQSNEYPGSTMKVMMLAAIDNNTFPGGEVFN 360
Sbjct 301 ILATTQRPFTFADTKEGIT+DFVWRDILYQSNEYPGSTMKVM LAAIDNNTFPGGEVFN 360
ILATTQRPFTFADTKEGITKDFVWRDILYQSNEYPGSTMKVMTLAAIDNNTFPGGEVFN 360

Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSELKIAD TIRDWDVN+GLT GRMMTF QGFA SSNVGM+LLEQKMGDATWLDYLNRFK 420
SSELKIADVTIRDWDVNDGLTTGRMMTFLQGFA LSSNVGMSLLEQKMGDATWLDYLNRFK 420

Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI 480
FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480

Query 481 SAIYDPNDQTARKSQKEIVGNPNVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYDPNDQTARKSQKEIVGNPNVSKDAASLTRTNMVLVGTDPVYGTMYNH TGKP +TVP 540
SAIYDPNDQTARKSQKEIVGNPNVSKDAASLTRTNMVLVGTDPVYGTMYNHQTGKPIITVP 540

Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYS +QL 600
GQNVAVKSGTAQIADEKNGGYLVGSTNYIFS VVTMNPENPDFILYVTVQQPEHYS AVQL 600

Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEF+NPILERASAMK+SLNLQ+ AK L+QV+ +S Y MPS+KDISPGDLAE LRRN+VQP 660
GEFSNPILERASAMKESLNLQSPAKNLDQVTTESSYAMPSIKDISPGDLAEALRRNIVQP 660

Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVLLISDKAEVDPMYGWTKEAETLAKWLNIELEF 720
Sbjct 661 IVVGTGTKIK +S EEGKNLAPNQVLL+LSDK EE+PDYMGWTK TAE +KWLNIEL F 720
IVVGTGTKIKETSVEEGKNLAPNQVLLLSDKVEEIPDYGWTKATAEAFSKWLNIELVF 720

Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721 +GSGSTVQKQDVRANTAIKDIKKITLTLGD 750
EGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

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Sbjct 721 EGS GSTVQKQDVRANTAIKDIKKITLTLGD 750

>dbj|BAD00909.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1345 bits (3481), Expect = 0.0, Method: Composition-based stats.
Identities = 693/750 (92%), Positives = 720/750 (96%), Gaps = 0/750 (0%)


Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTP	540
Sbjct	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Query	661	IVVGTGTHIKNSSAEEGNLAPNQVLLLSDKAEVDPMYGWTKEATLAKWLNIELEF	720
Sbjct	661	IVVGTGTHIKNSSAEEGNLAPNQVLLLSDKAEVDPMYGWTKEATLAKWLNIELEF	720
Query	721	QSG GSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	EGS GSTVQKQDVRANTAIKDIKKITLTLGD 750	


>dbj|BAD00907.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1344 bits (3478), Expect = 0.0, Method: Composition-based stats.
Identities = 691/750 (92%), Positives = 721/750 (96%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE	300

Sbjct	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEG+T+DFVWRDILYQSNYEPGSTMKVM LA++IDNNTFP GE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIAD TIRDWDVN+GLT GRMMTF QGFA SSNVGM+LLEQKMGD TWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSCKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTV	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVG PVS+DAASLRTNM+LVGTD+YGTMYNH TGKP +TV	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNV+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERASAMK+SLNLQ+ AK L+QV+ +S Y MPS+KDISPGDLAE LRRN+VQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVPMYGWTKETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIK +S EEGKNLAPNQVLL+LSDK EE+PDYMGW KETAET AKWL+IELEF	720
Query	721	QSGGSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLGD 750	

>pdb|1QME|A  Chain A, Penicillin-Binding Protein 2x (Pbp-2x)

 pdb|1QMF|A  Chain A, Penicillin-Binding Protein 2x (Pbp-2x) Acyl-Enzyme Complex
Length=702

Score = 1344 bits (3478), Expect = 0.0, Method: Composition-based stats.
Identities = 702/702 (100%), Positives = 702/702 (100%), Gaps = 0/702 (0%)

Query	49	GTGTRFGTDLAKEAKKVHQTTRTPVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT	108
Sbjct	1	GTGTRFGTDLAKEAKKVHQTTRTPVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT	60
Query	109	GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGGITYANMMSIKK	168
Sbjct	61	GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGGITYANMMSIKK	120
Query	169	ELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA	228
Sbjct	121	ELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA	180
Query	229	GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKY	288
Sbjct	181	GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKY	240
Query	289	MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI	348
Sbjct	241	MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI	300
Query	349	DNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKM	408
Sbjct	301	DNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKM	360
Query	409	DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFATAI	468
Sbjct	361	DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFATAI	420
Query	469	ANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSCKDAASLRTNMVLVGTDPVYGTMY	528
Sbjct	421	ANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSCKDAASLRTNMVLVGTDPVYGTMY	480
Query	529	NHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT	588
Sbjct	481	NHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT	540
Query	589	VQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGD	648
Sbjct	541	VQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGD	600
Query	649	LAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVPMYGWTKETAET	708
		LAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVPMYGWTKETAET	

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Sbjct 601 LAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAEVDPMYGWTKETAE 660
Query 709 TLAKWLNIELEFQGGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
        TLAKWLNIELEFQGGSGSTVQKQDVRANTAIKDIKKITLTLGD
Sbjct 661 TLAKWLNIELEFQGGSGSTVQKQDVRANTAIKDIKKITLTLGD 702
```

>pdb|1PYY|A Chain A, Double Mutant Pbp2x T338aM339F FROM STREPTOCOCCUS Pneumoniae
Strain R6 At 2.4 A Resolution
Length=702

Score = 1341 bits (3471), Expect = 0.0, Method: Composition-based stats.
Identities = 700/702 (99%), Positives = 700/702 (99%), Gaps = 0/702 (0%)

```
Query 49 GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT 108
Sbjct 1 GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT 60
Query 109 GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKK 168
Sbjct 61 GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKK 120
Query 169 ELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA 228
Sbjct 121 ELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA 180
Query 229 GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKY 288
Sbjct 181 GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKY 240
Query 289 MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI 348
Sbjct 241 MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGS KVMMLAAAI 300
Query 349 DNNTFPGGEVFNSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMG 408
Sbjct 301 DNNTFPGGEVFNSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMG 360
Query 409 DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAI 468
Sbjct 361 DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAI 420
Query 469 ANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSCKDAASLTRTNMVLVGTDPVYGTM 528
Sbjct 421 ANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSCKDAASLTRTNMVLVGTDPVYGTM 480
Query 529 NHSTGKPTVTVPQGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT 588
Sbjct 481 NHSTGKPTVTVPQGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT 540
Query 589 VQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGD 648
Sbjct 541 VQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGD 600
Query 649 LAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAEVDPMYGWTKETAE 708
Sbjct 601 LAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAEVDPMYGWTKETAE 660
Query 709 TLAKWLNIELEFQGGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 661 TLAKWLNIELEFQGGSGSTVQKQDVRANTAIKDIKKITLTLGD 702
```

>dbj|BAD00918.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1340 bits (3469), Expect = 0.0, Method: Composition-based stats.
Identities = 692/750 (92%), Positives = 718/750 (95%), Gaps = 0/750 (0%)

```
Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
```

Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFP GGGEVFN	360
Sbjct	301	ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERA AMKDSLNLQ+TAK L+QV+ QS Y MPS+KDISPGDLAE LRRN+VQP	660
Query	661	IVVGTGTGKIKNSSAEEGKNLAPNQVLLISDKAEVVPD MYGWTKETAE TLAKWLNIELEF	720
Sbjct	661	IVVGTGTGKIK SS EEG NLAPNQVLL+LSDKAEVVPD MYGWT KAEAFSKWLNIELVF	720
Query	721	QGS GSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	+GSGSTVQKQDVRANTAIKDIKKITLTLGD 750	

>dbj|BAD00910.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1336 bits (3458), Expect = 0.0, Method: Composition-based stats.
Identities = 690/750 (92%), Positives = 719/750 (95%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFP GGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSE KIADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVA+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660

```

-Query 661  IVVGTGTKIKNSSAEEGKNLAPNQVLLSLSDKAEVDPMYGWTKETAE TLAKWLNIELEF 720
Sbjct 661  IVVGTGTKIK SS EEG NLAPNQVLL+LSDKAEVDPMYGWT KAE +KWLNIE+ F 720
IVVGTGTKIKESSVEEGTNLAPNQVLLSLSDKAEVDPMYGWT KATAEAFSKWLNIEIVF 720

-Query 721  QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721  +GSGSTVQKQDVRANTAIKDIKKITLTLGD
EGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

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>dbj|BAD00923.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
dbj|BAD00924.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
dbj|BAD00934.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

```

Score = 1327 bits (3433), Expect = 0.0, Method: Composition-based stats.
Identities = 683/750 (91%), Positives = 716/750 (95%), Gaps = 0/750 (0%)

```

Query 1  MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1  MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

Query 61  EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61  EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

Query 121  KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121  KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF 180

Query 181  TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181  TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR 240

Query 241  LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVS AKTGE 300
Sbjct 241  LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAF EKVKGKYMTATLVS AKTGE 300

Query 301  ILATTQRPTFDADTKEGITEDFVWRDILYQS NYEPGSTMKVMMLAAIDNNTFP GGEVFN 360
Sbjct 301  ILATTQRPTF+ADTKEGITEDFVWRDILYQS NYEPGS MKVM LA++IDNNTFP GE FN 360

Query 361  SSELKIADATIRDWDVNEGLTGGRMMTF SQGF AHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361  SSEFKIADATTRDWDVNDGLTTGGMMTF LQGF AHSSNVGMSLLEQKMGDATWLDYLRFK 420

Query 421  FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421  FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI 480

Query 481  SAIYDPNDQTARKSQKEIVGNPVS KDAASLTRTNMVLVGTD PVYGTMYNHSTGKPTVTVP 540
Sbjct 481  SAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTD P+YGTMYNH TGK P +TVP 540

Query 541  GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541  GQNV A+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL 600

Query 601  GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601  GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP 660

Query 661  IVVGTGTKIKNSSAEEGKNLAPNQVLLSLSDKAEVDPMYGWTKETAE TLAKWLNIELEF 720
Sbjct 661  IVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PD MYGW KETAET AKWL+IELEF 720

Query 721  QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721  +GSGS VQKQDVR NTAIK+IKKITLTLGD
EGSGSVVQKQDVRTNTAIKNIKKITLTLGD 750

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>dbj|BAD00917.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

```

Score = 1324 bits (3427), Expect = 0.0, Method: Composition-based stats.
Identities = 680/750 (90%), Positives = 717/750 (95%), Gaps = 0/750 (0%)

```

Query 1  MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1  MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

Query 61  EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61  EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

Query 121  KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF 180

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- Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KGNNGITYANMM+IKKELE AEVKGIDF 180
Query 181 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGSKGNNGITYANMMAIKKELETAEVKGIDF 240
- Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Query 241 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
- Sbjct 241 LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE 300
Query 241 LGNIVPGTEQVSQ+T+DGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQQTVDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE 300
Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAIIDNNTFPGGEVFN 360
Sbjct 301 ILATTQRPTFDADTKEG+T+DFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN 360
Query 361 ILATTQRPTFDADTKEGLTKDFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFN 360
Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSE KIADAT RDWDVN+GLT G MMTF QGFHSSNVGM+LLEQKMGDATWLDYL RFK 420
Query 421 SSEFKIADATTRDWDVNDGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFK 420
Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTOMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI 480
Query 481 FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480
Query 481 SAIYDPNDQTARKSQKEIVGNPVSFDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYD N+Q+ RKSQKEIVGNPVS+K+AS TR +M+LVGTDP+YGTMYNH TGKP +TVP 540
Query 541 SAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRNHMILVGTDPVYGTMYNHSTGKPIITVP 540
Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNVA+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSGIQL 600
Query 601 GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPENPDFILYVTVQQPEHYSGIQL 600
Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPGDLAE LRRN+VQP 660
Query 661 GEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGDLAEALRRNLVQP 660
Query 661 IVVGTGTGIKNSSAEEGKNLAPNQVLLISDKAEVDPMYGWTKETATLAKWLNIELEF 720
Sbjct 661 IVVGTGTGIK+S EEGKNLAPNQVLL+LSDK EE+PDYMGW KETAT AKWL+IELEF 720
Query 721 IVVGTGTGIKETSVEEGKNLAPNQVLLLSDKVEEIPDYGWKKETATFAKWLDIELEF 720
Query 721 QGSGSTVQKQDVRANTAIKDIKITLTLGD 750
Sbjct 721 +GSGS VQKQDVR NTAIK+IKKI LTLGD 750
Query 721 EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750

```

>dbj|BAD00927.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1323 bits (3425), Expect = 0.0, Method: Composition-based stats.
Identities = 681/750 (90%), Positives = 715/750 (95%), Gaps = 0/750 (0%)

```

Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNNGITYANMMSIKKELEAAEVKGIDF 180
Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR 240
Query 241 LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQ+T+DGKDVTYTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGE 300
Query 301 LGNIVPGTEQVSQQTVDGKDVTYTTLSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGE 300
Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAIIDNNTFPGGEVFN 360
Sbjct 301 ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN 360
Query 361 ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFN 360
Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSE KIADAT RDWDVNEGLT G MMTF QGFHSSNVGM+LLEQKMGDATWLDYL RFK 420
Query 421 SSEFKIADATTRDWDVNEGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFK 420
Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTOMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI 480
Query 481 FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480
Query 481 SAIYDPNDQTARKSQKEIVGNPVSFDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYD N+Q+ RKSQKEIVGNPVS+K+AS TR +M+LVGTDP+YGTMYNH TGKP +TVP 540
Query 481 SAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRNHMILVGTDPVYGTMYNHSTGKPIITVP 540

```

```

Query   541  GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL  600
Sbjct   541  GQNVA+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSGIQL  600
Query   601  GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP  660
Sbjct   601  GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPGDLAEELRRN+VQP  660
Query   661  IVVGTGTHKIKNSSAEEGKNLAPNQVLLILSDKAEVDPMYGWTKEAETLAKWLNIELEF  720
Sbjct   661  IVVGAGTHKIKETSVEEGTNLAPNQVLLILSDKVEEIPDMYGWKKETAETFAKWLDIELEF  720
Query   721  QGSGSTVQKQDVRANTAIKDIKKITLTLGD  750
Sbjct   721  +GSGS VQKQDVR NTAIK+IKKI LTLGD  750

```

>dbj|BAD00913.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1318 bits (3410), Expect = 0.0, Method: Composition-based stats.
Identities = 677/750 (90%), Positives = 714/750 (95%), Gaps = 0/750 (0%)

```

Query   1    MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK  60
Sbjct   1    MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK  60
Query   61    EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN  120
Sbjct   61    EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN  120
Query   121   KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF  180
Sbjct   121   KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMM+IKKELE AEVKGIDF  180
Query   181   TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSMESSLNSILAGTDGIITYEKDR  240
Sbjct   181   TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSMESSLNSILAG DGIITYEKDR  240
Query   241   LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE  300
Sbjct   241   LGNIVPGTEQVSQQTVDGKDVTYTTLSSPLQSFMETQMDAFLEKVKGYMTATLVSAKTGE  300
Query   301   ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGVEFN  360
Sbjct   301   ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN  360
Query   361   SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGGDATWLDYLNRFK  420
Sbjct   361   SSEFKIADATTRDWDVNEGLTTGGMMTFLQGFHSSNVGMSLLEQKMGGDATWLDYLKRFK  420
Query   421   FGVPTREFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI  480
Sbjct   421   FGVPTREFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI  480
Query   481   SAIYDPNDQTARKSQKEIVGNPVSKEAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP  540
Sbjct   481   SAIYD N+Q+ RKSQKEIVGNPVSKEAASLRTNMILVGTDPVYGTMYNHSTGKPTVTVP  540
Query   541  GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL  600
Sbjct   541  GQNVA+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSGIQL  600
Query   601  GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP  660
Sbjct   601  GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP  660
Query   661  IVVGTGTHKIKNSSAEEGKNLAPNQVLLILSDKAEVDPMYGWTKEAETLAKWLNIELEF  720
Sbjct   661  IVVGTHKIKETSVEEGTNLAPNQVLLILSDKVEEIPDMYGWKKETAETFAKWLDIELEF  720
Query   721  QGSGSTVQKQDVRANTAIKDIKKITLTLGD  750
Sbjct   721  +GSGS VQKQDVR NTAIK+IKKI LTLGD  750

```

>dbj|BAD00938.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1316 bits (3407), Expect = 0.0, Method: Composition-based stats.
Identities = 676/750 (90%), Positives = 713/750 (95%), Gaps = 0/750 (0%)

```

Query   1    MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK  60
Sbjct   1    MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK  60

```

```
Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNL QVSFGAKNGITYANMM+IKKELE AEVKGIDF 180

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR 240

Query 241 LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQ+T+DGKDVYTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGE 300

Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFP GGGEVFN 360
Sbjct 301 ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS KVMMLA++IDNNTFP GE FN 360

Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSE KIADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK 420

Query 421 FGVPTREFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTREFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480

Query 481 SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGYTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTD+YGYTMYNH TGKP +TVP 540

Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL 600
Sbjct 541 GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPENPDFILYVTVQQPEHYSIGIQL 600

Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQSPYMPSPVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP 660

Query 661 IVVGTGTHKIKNSSAEEGKNLAPNQVLLLSDKAEVDPMYGWTAKETAETLAKWLNIELEF 720
Sbjct 661 IVVGTGTHKIKETSVEEGTNLAPNQVLLLSDKVEEIPDMYGWKKETAETFAKWL DIELEF 720

Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721 +GSGS VQKQDVR NTAIK+IKKI LTLGD 750
EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750
```

>dbj|BAD00922.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1316 bits (3405), Expect = 0.0, Method: Composition-based stats.
Identities = 678/750 (90%), Positives = 713/750 (95%), Gaps = 0/750 (0%)

```
Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIGTGTRFGTDLAK 60
Sbjct 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVIGTGTRFGTDLAK 60

Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELE AEVKGIDF 180

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR 240

Query 241 LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQ+T+DGKDVYTTISS LQSFMETQMDAF EKVKGKYMTATLVSAKTGE 300

Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFP GGGEVFN 360
Sbjct 301 ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN 360

Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSE KIADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK 420

Query 421 FGVPTREFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTREFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480
```

```

- Query 481  SAIYDPNDQTARKSQKEIVGNPVSKDAA SLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481  SAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP 540
SAIYDTNNQSVRKSQKEIVGNPVSKEAASTTRNHMILVGTDPPLYGTMYNHYTGKPIITVP

- Query 541  GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541  GQNVA+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSGIQL 600
GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPENPDFILYVTVQQPEHYSGIQL

Query 601  GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601  GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP 660
GEFATPILERASAMKESLNLQSPAKNLDKVTTESYAMP SIKDISPGELAEALRRNIVQP

Query 661  IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPMYGWT KETAETLAKWLNIELEF 720
Sbjct 661  IVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PD MYGW KETAET AKWL+IELEF 720
IVVGTGTKIKETSVEEGTNLAPNQVLLLSDKVEEIPD MYGWKKETAETFAKWLDIELEF

Query 721  QGSGSTVQKQDV RANTAIKDIKKITLTLGD 750
Sbjct 721  +GSGS VQKQDVR NTAIK+IKKI LTLGD 750
EGSGSVVQKQDV RTNTAIKNIKKIKLTLGD 750

```

>dbj|BAD00925.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1315 bits (3403), Expect = 0.0, Method: Composition-based stats.
Identities = 676/750 (90%), Positives = 712/750 (94%), Gaps = 0/750 (0%)

```

Query 1  MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1  MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVIIGTGTRFGTDLAK 60
MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAVFLVNFAVIIGTGTRFGTDLAK

Query 61  EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61  EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN

Query 121  KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121  KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELE AEVKGIDF 180
KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELETAEVKGIDF

Query 181  TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181  TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR 240
TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGKDGIITYEKDR

Query 241  LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241  LGNIVPGTEQVSQ+T+DGKDVYTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGE 300
LGNIVPGTEQVSQQTVDGKDVYTTLSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGE

Query 301  ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAIDNNTFP GGEVFN 360
Sbjct 301  ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS KVMMLA++IDNNTFP GE FN 360
ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGS AFKVMMLASSIDNNTFPSGEYFN

Query 361  SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361  SSE KIADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK 420
SSEFKIADATTRDWDVNEGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRFK

Query 421  FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAF TA IANDGVMLEPKFI 480
Sbjct 421  FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTA IANDGVMLEPKFI 480
FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTA IANDGVMLEPKFI

Query 481  SAIYDPNDQTARKSQKEIVGNPVS KDAA SLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481  SAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP 540
SAIYDTNNQSVRKSQKEIVGNPVSKEAASTTRNHMILVGTDPPLYGTMYNHYTGKPIITVP

Query 541  GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541  GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQ 600
GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENPDFILYVTVQQPEHYSGIQS

Query 601  GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601  GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP 660
GEFATPILERASAMKESLNLQSPAKNLDKVTTESYAMP SIKDISPGELAEALRRNIVQP

Query 661  IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPMYGWT KETAETLAKWLNIELEF 720
Sbjct 661  IVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PD MYGW KETAET AKWL+IELEF 720
IVVGTGTKIKETSVEEGTNLAPNQVLLLSDKVEEIPD MYGWKKETAETFAKWLDIELEF

Query 721  QGSGSTVQKQDV RANTAIKDIKKITLTLGD 750
Sbjct 721  +GSGS VQKQDVR NTAIK+IKKI LTLGD 750
EGSGSVVQKQDV RTNTAIKNIKKIKLTLGD 750

```

>dbj|BAD00926.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1315 bits (3402), Expect = 0.0, Method: Composition-based stats.
Identities = 676/750 (90%), Positives = 714/750 (95%), Gaps = 0/750 (0%)

- Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTK+VIRYATKNRKSPAENRRRVGKSLSLLSVVFVFA+FLVNFAVIIGTGTRFGTDLAK	60
- Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE	300
Sbjct	241	+GNIVPGTE VSQ+T+DGKDVTYTT+SSPLQSFMETQMDAF EKVKGKMYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTF GE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSE KIADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKEAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPVSKEAAS TR +M+LVGTDP+YGTMYNH TGKP +TVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVA+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLISDKAEVVPDYGWTKETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIK+S EEG NLAPNQVLL+LSDK EE+PDYGW KETAET AKWL+IELEF	720
Query	721	QGSGSTVQKQDVRRNTAIKDIKKITLTLGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLGD 750	

>gb|AAFI17268.1|AF210758_1 penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1313 bits (3398), Expect = 0.0, Method: Composition-based stats.
Identities = 675/750 (90%), Positives = 713/750 (95%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KNGITYANMMSIKKELEAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE	300
Sbjct	241	+GNIVPGTE VSQ+T+DGKDVTYTT+SSPLQSFMETQMDAF EKVKGKMYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTF GE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420

Sbjct	361	SSEFKIADATTRDWDVNDGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRKF	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKEAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPVSKEAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVA+KSGTAQIADEKNGGYLVGT T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLSDKAEVPMYGTWKETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIK+S EEG NLAPNQVLL+LSDK EE+PDYMGW KETAET AKWL+IELEF	720
Query	721	QGSSTVQKQDVRRNTAIKDIKKITLTLGD	750
Sbjct	721	EGSGSVVQKQDVRRNTAIKDIKKITLTLGD	750

>gb|AAFI7270.1|AF210760_1 penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1312 bits (3396), Expect = 0.0, Method: Composition-based stats.
Identities = 673/750 (89%), Positives = 713/750 (95%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSAPENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSAPENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMAIKKELETAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKMYTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKMYTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGEVFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRKF	420
Sbjct	361	SSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYLRKF	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKEAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPVSKEAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVA+KSGTAQIADEKNGGYLVGT T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG++AE LRRN+VQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLSDKAEVPMYGTWKETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIK+S EEG NLAPNQVLL+LSDK EE+PDYMGW KETAET AKWL+IELEF	720
Query	721	QGSSTVQKQDVRRNTAIKDIKKITLTLGD	750
Sbjct	721	EGSGSVVQKQDVRRNTAIKDIKKITLTLGD	750

>dbj|BAD00932.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1312 bits (3396), Expect = 0.0, Method: Composition-based stats.
Identities = 673/750 (89%), Positives = 712/750 (94%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQQTVDGKDVYTTLSPLQSFMETQMDAFLEKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFP GG EVFN	360
Sbjct	301	ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS KVMMLA++IDNNTFP GE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSE KIADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPVSK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL	600
Sbjct	541	GQNVAKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENPDFILYVTVQQPEHITSVQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEF+NPILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVVPDYGWTKETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIK+S EEG NLAPNQVLL+LSDK EE+PDYGW KETAET AKWL+IELEF	720
Query	721	QSGSGTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLGD 750	

>gb|AAF17269.1|AF210759_1 penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1312 bits (3395), Expect = 0.0, Method: Composition-based stats.
Identities = 674/750 (89%), Positives = 712/750 (94%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQVSQQTVDGKDVYTTLSPLQSFMETQMDAF+KVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFP GG EVFN	360

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- Sbjct 301 ILATTQRPTF+ADTKEGITEDFVWRDILYQSNEYEPGS KVM LA++IDNNTFP GE FN 360
ILATTQRPTFNADTKEGITEDFVWRDILYQSNEYEPGSFAKVMTLASSIDNNTFPSGEYFN
Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
SSE KIADAT RDWDVN GLT G MMTF SQGFAHSSNVG +LLEQKMGDATWLDYL RFK
- Sbjct 361 SSEFKIADATTRDWDVNAGLTTGGMMTFSQGFAHSSNVGTSLLEQKMGDATWLDYLNRFK 420
Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480
Query 481 SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
SAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTD P+YGTMYNH TGKP +TVP
Sbjct 481 SAIYDTNNQSGRKSQKEIVGNPVSKEAASSTRNHMILVGTDPVYGTMYNHYTGPPIITVP 540
Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL 600
GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEH+SGIQL
Sbjct 541 GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENPDFILYVTVQQPEHFSIGIQL 600
Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP
Sbjct 601 GEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQP 660
Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPMYGWTKETAE TLAKWLNIELEF 720
IVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PDYMGW KETAE AKWL+IELEF
Sbjct 661 IVVGTGTKIKETSVEEGTNLAPNQVLLLSDKVEEIPDYGWKKETAE TFAKWLDIELEF 720
Query 721 QGSGSTVQKQDV RANTAIKDIKKITLTLGD 750
+GSGS VQKQDVR NTAIK+IKKI LTLGD
Sbjct 721 EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750

```

>dbj|BAD00936.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1312 bits (3395), Expect = 0.0, Method: Composition-based stats.
Identities = 675/750 (90%), Positives = 712/750 (94%), Gaps = 0/750 (0%)

```

Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVFVFA+FLVNFAVIIGTGTRFGTDLAK 60
Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAEVKGIDF 180
Query 181 TTSPNRSYPNGQFASSFIGLAQLHENE DGSKSLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENE DGSKSLGTSGMESSLNSILAG DGIITYEKDR 240
Query 241 LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQQTVDGKDVTYTTISSTLQSFMETQMDAFLEKVKGYMTATLVSAKTGE 300
Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYEPGSTMKVMMLAAIDNNTFPGGEVFN 360
Sbjct 301 ILATTQRPTF+ADTKEGITEDFVWRDILYQSNEYEPGS MKVM LA++IDNNTFP GE FN 360
Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
SSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL+RFK
Sbjct 361 SSEFKIADATTRDWDVNDGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLSRFK 420
Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480
Query 481 SAIYDPNDQTARKSQKEIVGNPVS KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
SAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR +M+LVGTD P+YGTMYNH TGKP +TVP
Sbjct 481 SAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRNHMILVGTDPVYGTMYNHYTGPPIITVP 540
Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQL 600
GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSIGIQL
Sbjct 541 GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENPDFILYVTVQQPEHYSIGIQL 600
Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP
Sbjct 601 GEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQP 660
Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPMYGWTKETAE TLAKWLNIELEF 720
IVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PDYMGW KETAE AKWL+IELEF
Sbjct 661 IVVGTGTKIKETSVEEGTNLAPNQVLLLSDKVEEIPDYGWKKETAE TFAKWLDIELEF 720

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Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
+GSGS VQKQDVR NTAIK+IKKI LTLGD
Sbjct 721 EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750

```

>gb|AAL77081.1|AF468152_1 penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1307 bits (3382), Expect = 0.0, Method: Composition-based stats.
Identities = 667/750 (88%), Positives = 711/750 (94%), Gaps = 0/750 (0%)

```

Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTKR+ R+A +NRKSPAENR+ VGK +SLL+V +FA+FLVNFAVIIG+G++FGTDL K
MKWTKRITRFAIRNRKSPAENRKIVGKYISLLAVVLFAVFLVNFAVIIGSGSKFGTDLVK 60

Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQ TRTPAKRGTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFN
EAKKVHQITRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFN 120

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEAYVKEQLAQPNLTQVSFGAKGNGITYANMMAIKKDKDASVEGIDF 180

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR
TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGKDGIIITYEKDR 240

Query 241 LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQ+T+DGKDVYTTISS LQSFMETQM+AFQEKVKGKYMTATLVSAKTGE
LGNIVPGTEQVSQQTVDGKDVYTTISSSTLQSFMETQMNAFQEKVKGKYMTATLVSAKTGE 300

Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYEPGSTMKVMMLAAAI DNNTFPGGEVFN 360
Sbjct 301 ILATTQRPTFDADTKEG+T+DFVWRDILYQSNEYEPGSTMKVM LAAAI DNNTFPGGEVFN
ILATTQRPTFDADTKEGLTKDFVWRDILYQSNEYEPGSTMKVMTLAAAI DNNTFPGGEVFN 360

Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSELKIAD TIRDWDVNEGLTGGRMMTFSQGF A SSNVGMTLLEQKMGDATWLDYLNRFK
SSELKIADVTIRDWDVNEGLTGGRMMTFSQGFALSSNVGMTLLEQKMGDATWLDYLNRFK 420

Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI
FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480

Query 481 SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDVPYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYD N+Q+ RKSQKEIVG PVS+DAASLRTNM+LVGTD+YGTMYNH TGKP +TVP
SAIYDTNNQSVRKSQKEIVGKPVSEDAASLRTNMILVGTDPLYGTMYNHQTGKPIITVP 540

Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL
GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPANPDFILYVTVQQPEHYSGIQL 600

Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEFANPILERA AMKDSLNLQ+TAK L+QV+ QS Y MPS+KDISPGDLAE LRRN+VQP
GEFANPILERAVAMKDSLNLQSTAKTLBQVTNQSAYAMPSIKDISPGDLAEALRRNIVQP 660

Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPMYGWTKETAEFLAKWLNIELEF 720
Sbjct 661 IVVGTGTKIK SS EEG NLAPNQVLL+LSDKAEVDPMYGWTK TAE +KWLNIEL F
IVVGTGTKIKESSVEEGTNLAPNQVLLLSLKAEVDPMYGWTKATAEAFSKWLNIELVF 720

Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
+GSGSTVQKQDVRANTAIKDIKKI LTLGD
Sbjct 721 EGSGSTVQKQDVRANTAIKDIKKIKLTLGD 750

```

>dbj|BAD00939.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1307 bits (3382), Expect = 0.0, Method: Composition-based stats.
Identities = 670/750 (89%), Positives = 711/750 (94%), Gaps = 0/750 (0%)

```

Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTK+VIRYATKNRKSPAENRRRVGKSLSLSVFVFA+FLVNFAVIIGTGTRFGTDLAK
MKWTKKVIRYATKNRKSPAENRRRVGKSLSLSVFVFAVFLVNFAVIIGTGTRFGTDLAK 60

Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQ TRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN
EAKKVHQITRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KNGNGITYANMM+IKKELE AEVKGIDF
KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGSKGNGITYANMMAIKKELETAEVKGIDF 180

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR
TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240

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Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	+GNIVPGTE VSQ+T+DGKDVYTT+SSPLQSFMETQMDAF +KVKGYMTATLVSAKTGE VGNIVPGTELVSQQTVDGKDVYTTLSSPLQSFMETQMDAFLQKVKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS KVMMLA++IDNNTFP GE FN ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSFAKVMMLASSIDNNTFPSGEYFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSE KIADAT RDWDVNEGLT G MMTF QGFHSSNVG +LLEQKMGDATWLDYL RFK SSEFKIADATTRDWDVNEGLTTGGMMTFLQGFHSSNVGTSLLEQKMGDATWLDYLRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPNVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPNVSK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP SAIYDTNNQSVRKSQKEIVGNPNVSKEAASSTRNHMILVGTDPPLYGTMYNHYTGKPIITVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL GQNVAVKSGTAQIADEKNGGYLVGSTNYIFS SVVTMNPENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP GEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLILSDKAEVPMYGTWKETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIK +S EEG NLAPNQVL+LSDK EE+PDYMGW KETAET AKWL+IELEF IVVGTGTKIKETSVEEGTNLAPNQVLLLSDKVEEIPDYGWKKETAETFAKWLIDIELEF	720
Query	721	QGS GSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLGD EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750	

>dbj|BAD00935.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1306 bits (3380), Expect = 0.0, Method: Composition-based stats.
Identities = 667/750 (88%), Positives = 715/750 (95%), Gaps = 0/750 (0%)

Query	1	MKWTKR VIRYATKNRKSPAENRRRVGKSLSLLSV FVFAIFLVNFAVIIGTGTRFGTDLAK	60
Sbjct	1	MKWTKR VIRYATKNRKSPAENRRRVGKSLSLLSV FVFAIFLVNFAVIIGTGTRFGTDLAK MKWTKR VIRYATKNRKSPAENRRRVGKSLSLLSV FVFAIFLVNFAVIIGTGTRFGTDLAK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KNGNGITYANMMSIKK+LE A+V+GIDF KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGSKGNGITYANMMSIKKDLETAKVEGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENE DGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNG+FASSFIGLAQLHENE DGSKSL+GTSG+ESSLNS+LAGTDGIITYEKDR TTSPNRSYPNGKFASSFIGLAQLHENE DGSKSLIGTSGVESSLNSLLAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQV+++T++GKDVYTT+SSPLQSFME+QMDAFQEK+KGKGYMTATLVSAKTGE LGNIVPGTEQVTRQTVNGKDVYTTLSSPLQSFMESQMDAFQEKLGKGYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSE KIADAT RDWDVNEGLT G MMTF QGFHSSNVGM+LLEQKMGDATWLDYL RFK SSEFKIADATTRDWDVNEGLTTGGMMTFLQGFHSSNVGMSLLEQKMGDATWLDYLRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPNVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPNVSK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP SAIYDTNNQSVRKSQKEIVGNPNVSKEAASSTRNHMILVGTDPPLYGTMYNHYTGKPIITVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL GQNVAVKSGTAQIADEKNGGYLVGSTNYIFS SVVTMNPENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP GEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQP	660

```

* Query 661  IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPMDYGWTKETAETLAKWLNIELEF 720
  Sbjct 661  IVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PMDYGW KETAET AKWL+IELEF
  IVVGTGTKIKETSVEEGTNLAPNQVLLLSDKVEEIPMDYGWKKETAETFAKWLIDIELEF 720

- Query 721  QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
  Sbjct 721  +GSGS VQKQDVR NTAIK+IKKI LTLGD
  EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750

```

>dbj|BAD00906.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1305 bits (3378), Expect = 0.0, Method: Composition-based stats.
Identities = 669/750 (89%), Positives = 710/750 (94%), Gaps = 0/750 (0%)

```

Query 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

Query 61     EAKKVHQTTTRTVPAPKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61     EAKKVHQTTTRTVPAPKRGTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFN
EAKKVHQTTTRTVPAPKRGTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFN 120

Query 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFG+KGNGITYANMM+IKKELE AEVKGIDF
KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGSKGNGITYANMMAIKKELETAEVKGIDF 180

Query 181    TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNILAGTDGIITYEKDR 240
Sbjct 181    TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLN ILAGTDGIITYEKDR
TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNRIILAGTDGIITYEKDR 240

Query 241    LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGE 300
Sbjct 241    LGNIVPGTEQVSQ+T+DGKDVYTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGE
LGNIVPGTEQVSQQTVDGKDVYTTLSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGE 300

Query 301    ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAIIDNNTFPGGVEFN 360
Sbjct 301    ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN
ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFN 360

Query 361    SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361    SSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK
SSEFKIADATTRDWDVNDGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRFK 420

Query 421    FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421    FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI
FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480

Query 481    SAIYDPNDQTARKSQKEIVGNPVSKEAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481    SAIYD N+Q+ RKSQKEIVGNPVSKEAAS TR +M+LVGTDP+YGTMYNH TGKP +TVP
SAIYDTNNQSVRKSQKEIVGNPVSKEAASLRTNMHMLVGTDPVYGTMYNHYTGKPIITVP 540

Query 541    GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541    GQNV+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL
GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPANPDFILYVTVQQPEHYSGIQL 600

Query 601    GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601    GEFATPILERASAMKDSLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP
GEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQP 660

Query 661    IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVDPMDYGWTKETAETLAKWLNIELEF 720
Sbjct 661    IVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PMDYGW KETAET AKWL+IELEF
IVVGTGTKIKETSVEEGTNLAPNQVLLLSDKVEEIPMDYGWKKETAETFAKWLIDIELEF 720

Query 721    QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721    +GSGS VQKQDVR NTAIK+IKKI LTLGD
EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750

```

>dbj|BAD00937.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1303 bits (3373), Expect = 0.0, Method: Composition-based stats.
Identities = 664/750 (88%), Positives = 711/750 (94%), Gaps = 0/750 (0%)

```

Query 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1      MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

Query 61     EAKKVHQTTTRTVPAPKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61     EAKKVHQ TTTRTVPAPKRGTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFN
EAKKVHQITRTVPAPKRGTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFN 120

Query 121    KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121    KVAEVFHKYLDME+YV+EQL+QPNL QVSFGAKGNGITYANMM+IKK+L+ A V+GIDF
KVAEVFHKYLDMEAYVKEQLAQPNLTQVSFGAKGNGITYANMMAIKKDLKDASVEGIDF 180

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- Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSG+ESSLN+ILAGTDGIITYEKDR 240

- Query 241 LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241 +GNIVPGTE VSQ+T+DGKDVTYTT+SSPLQSFMETQMDAF EKVKGKGYMTATLVSAKTGE 300
VGNIVPGTELVSQQTVDGKDVTYTTLSSPLQSFMETQMDAFLEKVKGKGYMTATLVSAKTGE 300

Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFP GGGEVFN 360
Sbjct 301 ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN 360
ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFN 360

Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSEFKIADATTRDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK 420
SSEFKIADATTRDWDVNEGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLNRFK 420

Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI 480
FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480

Query 481 SAIYDPNDQTARKSQKEIVGNPVSKDAAASLRTNMMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYD N+Q+ RKSQKEIVGNPVS+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP 540
SAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRNHMILVGTDPVYGTMYNHSTGKPIITVP 540

Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNVA+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSGIQL 600
GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPANPDFILYVTVQQPEHYSGIQL 600

Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEF PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPGDLAEELRRN+VQP 660
GEFVTPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGDLAEELRRNIVQP 660

Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVLLISDKAEVDPMYGWTKETAE TLAKWLNIELEF 720
Sbjct 661 IV+G GTKIKN+S EEGKNLAPNQVLL+LSDK EE+PDYMGWTK TAE +KWLNIELEF 720
IVIGAGTKIKNASIEEGKNLAPNQVLLLSDKVEEIPDYGWTKTAEAFSKWLNIELEF 720

Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721 +GSGSTVQKQDVRANTAIKDIKKITLTLGD 750
EGSGSTVQKQDVRANTAIKDIKKITLTLGD 750

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>pdb|1RP5|A Chain A, Pbp2x From Streptococcus Pneumoniae Strain 5259 With Reduced Susceptibility To Beta-Lactam Antibiotics

pdb|1RP5|B Chain B, Pbp2x From Streptococcus Pneumoniae Strain 5259 With Reduced Susceptibility To Beta-Lactam Antibiotics

emb|CAE53270.1| penicillin-binding protein 2x [Streptococcus pneumoniae] Length=702

Score = 1297 bits (3357), Expect = 0.0, Method: Composition-based stats.
Identities = 674/702 (96%), Positives = 688/702 (98%), Gaps = 0/702 (0%)

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Query 49 GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT 108
Sbjct 1 GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT 60
GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT

Query 109 GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKK 168
Sbjct 61 GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKK 120
GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKK

Query 169 ELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA 228
Sbjct 121 ELEAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA 180
ELEAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA

Query 229 GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGY 288
Sbjct 181 GTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVTYTTISSPLQSFMETQMDAFQEKVKGY 240
GTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDVTYTTISSPLQSFMETQMDAFQEKVKGY

Query 289 MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI 348
Sbjct 241 MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI 300
MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI

Query 349 DNNTFP GGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKM 408
Sbjct 301 DNNTFP GGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKM 360
DNNTFP GGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKM

Query 409 DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAI 468
Sbjct 361 DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIA S+FGQGISVTQTQM+RAFTAI 420
DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAMSAFGQGISVTQTQMLRAFTAI

Query 469 ANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAAASLRTNMMVLVGTDPVYGTMY 528
Sbjct 421 ANDGVMLEPKFIS+YDPNDQ+ RKSQKEIVGNPVS+AAS+TR +MV+VGTDY YGTMY 480
ANDGVMLEPKFISALYDPNDQSVRKSQKEIVGNPVSKEAASVTRDHMMVMVGTDPYGTMY

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Query 529 NHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT 588
Sbjct 481 NHSTGK TV VPGQNVALKSGTA+IADEKNGGYL G T+ IFS VSM PAENPDFILYVT 540
NHSTGKATVNVPGQNVALKSGTAEIADEKNGGYLTGSTNNIFSVSMHPAENPDFILYVT

Query 589 VQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGD 648
Sbjct 541 VQQPEHYSGIQLGEFANPILERASAMK+SLNLQTTAKALEQVSQQSPYPMPSVKDISPGD 600
VQQPEHYSGIQLGEFANPILERASAMKESLNLQTTAKALEQVSQQSPYPMPSVKDISPGD

Query 649 LAEELRRNLVQPIVVGTGTGIKKNSSAEEGKNLAPNQQVLILSDKAEVPMYGTKETAE 708
Sbjct 601 LAEELRRNLVQPIVVGTGTGIKKNSSAEEGKNLAPNQQVLILSDKAEVPMYGTKETAE 660
LAEELRRNLVQPIVVGTGTGIKKNSSAEEGKNLAPNQQVLILSDKAEVPMYGTKETAE

Query 709 TLAKWLNIELEFQSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 661 TFAKWLNIELEFEGSGSTVQKQDVRANTAIKDIKKIKLTLGD 702
T AKWLNIELEF+GSGSTVQKQDVRANTAIKDIKKI LTLGD

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>dbj|BAD00914.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
dbj|BAD00930.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
dbj|BAD00931.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
dbj|BAD00933.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

```

Score = 1296 bits (3354), Expect = 0.0, Method: Composition-based stats.
Identities = 662/750 (88%), Positives = 707/750 (94%), Gaps = 0/750 (0%)

```

Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIG+G++FGTDL K 60
MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAVFLVNFAVIIGSGSKFGTDLVK

Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQ TRTPAKRGTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFN 120
EAKKVHQITRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFN

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEAYVKEQLSQPNLTQVSFGAKGNGITYANMMAIKKELETAEVKGIDF 180
KVAEVFHKYLDMEAYVKEQLSQPNLTQVSFGAKGNGITYANMMAIKKELETAEVKGIDF

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAG DGIITYEKDR 240
TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGKDGIIITYEKDR

Query 241 LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQQTVDGKDVTYTTLSPLQSFMETQMDAFLEKVKGKMYMTATLVSAKTGE 300
LGNIVPGTEQVSQQTVDGKDVTYTTLSPLQSFMETQMDAFLEKVKGKMYMTATLVSAKTGE

Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGVEFN 360
Sbjct 301 ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN 360
ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFN

Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK 420
SSEFKIADATTRDWDVNDGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFK

Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI 480
FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI

Query 481 SAIYDPNDQTARKSQKEIVGNPVSCKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYD N+Q+ RKSQKEIVGNPVSCK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVP 540
SAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRNHMILVGTDPVYGTMYNHYTGKPIITVP

Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNV+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL 600
GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENPDFILYVTVQQPEHYSGIQL

Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP 660
GEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQP

Query 661 IVVGTGTGIKKNSSAEEGKNLAPNQQVLILSDKAEVPMYGTKETAE TLAKWLNIELEF 720
Sbjct 661 IVVGTGTGIKETSVEEGTNLAPNQQVLLSLDKVEEIPMYGWKKETAETFAKWLDIELEF 720
IVVGTGTGIKETSVEEGTNLAPNQQVLLSLDKVEEIPMYGWKKETAETFAKWLDIELEF

Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721 EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750
+GSGS VQKQDVR NTAIK+IKKI LTLGD

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```

>dbj|BAD00928.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

```


Score = 1294 bits (3348), Expect = 0.0, Method: Composition-based stats.
Identities = 662/750 (88%), Positives = 706/750 (94%), Gaps = 0/750 (0%)

```

Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60

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Sbjct	1	MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFA+FLVNFAVIIG+G++FGTDL K MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFAVFLVNFAVIIGSGSKFGTDLVK	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN EAKKVHQ TRTPAKRGTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFN	120
Sbjct	61	EAKKVHQITRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDF KVAEVFHKYLDME+YV+EQLSQPNL QVSFGAKNGITYANMM+IKKELE AEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEAYVKEQLSQPNLTQVSFGAKNGITYANMMAIKKELETAEVKGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAG DGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGKDGIIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSATKGE LGNIVPGTEQVSQ+T+DGKDVYTT+SSPLQSFMETQMDAF EKVKGKGYMTATLVSATKGE	300
Sbjct	241	LGNIVPGTEQVSQQTVDGKDVYTTLSPLQSFMETQMDAFLEKVKGKGYMTATLVSATKGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFN ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS KVM LA++IDNNTFP GE FN	360
Sbjct	301	ILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAFKVMTLASSIDNNTFPSGEYFN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK SSE KIADAT RDWDVN GLT G MMTFSQGFAHSSNVG +LLEQKMGDATWLDYL RFK	420
Sbjct	361	SSEFKIADATTRDWDVNAGLTTGGMMTFSQGFAHSSNVGTSLLEQKMGDATWLDYLKRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP SAIYD N+Q+ RKSQKEIVG PVS+DAASLRTNM+LVGTDP+YGTMYNH TGKP +TVP	540
Sbjct	481	SAIYDTNNQSVRKSQKEIVGKPVSEDAASLRTNMILVGTDPVYGTMYNHYTGKPIITVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSQIQL GQNV+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEH+SQIQL	600
Sbjct	541	GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPANPDFILYVTVQQPEHFSQIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQP GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Sbjct	601	GEFATPILERASAMKESLNLQSPAKNLDKVTTESYAMPSIKDISPGELAEALRRNIVQP	660
Query	661	IVVGTGTTIKNSSAEEGKNLAPNQVLLISDKAEVPMYGTWKETAETLAKWLNIELEF IVVGTGTTIK +S EEG NLAPNQVLL+LSDK EE+PMYGW KETAET AKWL+IELEF	720
Sbjct	661	IVVGTGTTIKETSVEEGTNLAPNQVLLLSDKVEEIPMYGWKKETAETFAKWLDIELEF	720
Query	721	QSGGSTVQKQDVRRANTAIKDIKKITLTLGD 750 +GSGS VQKQDVR NTAIK+IKKI LTLGD	
Sbjct	721	EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750	

>pdb|1PMD|  Chain , Penicillin-Binding Protein 2x (Pbp-2x)
Length=675

Score = 1294 bits (3348), Expect = 0.0, Method: Composition-based stats.
Identities = 675/675 (100%), Positives = 675/675 (100%), Gaps = 0/675 (0%)

Query	76	RGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEES RGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEES	135
Sbjct	1	RGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEES	60
Query	136	YVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFAS YVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFAS	195
Sbjct	61	YVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFAS	120
Query	196	SFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRT SFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRT	255
Sbjct	121	SFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRT	180
Query	256	MDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSATKGEILATTQRPTFDADTK MDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSATKGEILATTQRPTFDADTK	315
Sbjct	181	MDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSATKGEILATTQRPTFDADTK	240
Query	316	EGITEDFVWRDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWD EGITEDFVWRDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWD	375
Sbjct	241	EGITEDFVWRDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWD	300
Query	376	VNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAG VNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAG	435
Sbjct	301	VNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAG	360
Query	436	QLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQ QLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQ	495
Sbjct	361	QLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQ	420

```

Query 496 KEIVGNPVSFDAASLRTNMLVVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIAD 555
Sbjct 421 KEIVGNPVSFDAASLRTNMLVVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIAD 480

Query 556 EKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK 615
Sbjct 481 EKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK 540

Query 616 DSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAE 675
Sbjct 541 DSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAE 600

Query 676 EGKNLAPNQVVLILSDKAEVDPMYGWTKETAE TLAKWLNIELEFQSGSGSTVQKQDVRAN 735
Sbjct 601 EGKNLAPNQVVLILSDKAEVDPMYGWTKETAE TLAKWLNIELEFQSGSGSTVQKQDVRAN 660

Query 736 TAIKDIKKITLTLGD 750
Sbjct 661 TAIKDIKKITLTLGD 675

```

>gb|AAC45547.1| low-affinity penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1284 bits (3323), Expect = 0.0, Method: Composition-based stats.
Identities = 654/750 (87%), Positives = 704/750 (93%), Gaps = 0/750 (0%)

```

Query 1 MKWTKRVIRYATKNRKS PAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTKRITRFAIRNRKS PAENRRKIVGKYISLLAVVLFVAVFLVNFAVIIGSGSKFGTDLVK 60

Query 61 EAKKVHQTRTVP AKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQITRTVP AKRGTIYDRNGVPIAEDATSYNVYAVIDDKYKSATGKILYVEDAQFN 120

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLQVVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEESYVREQLSQPNLQVVSFG+KNGITYANMM+IKKELE AEVKGIDF 180

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR 240

Query 241 LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241 VGNIVPGTELVSQQTVDGKDVTYTTLSPLQSFMETQMDAFLEKVKGYMTATLVSAKTGE 300

Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN 360
Sbjct 301 ILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FN 360

Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSE KIADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFK 420

Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI 480

Query 481 SAIYDPNDQTARKSQKEIVGNPVSFDAASLRTNMLVVGTDVPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYD N+Q+ RKSQKEIVGNPVSK+AAS TR +M+LVGTD+YGTMYNH TGKP +TVP 540

Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPENPDFILYVTVQQPEHYSGIQL 600

Query 601 GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP 660

Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVVLILSDKAEVDPMYGWTKETAE TLAKWLNIELEF 720
Sbjct 661 IVVGTGTKIK+ S EEG NLAPNQVVL+LSDK EE+PDYMGW KETAET AKWL+IELEF 720

Query 721 QGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct 721 EGSGSVVQKQDVRTNTAIKNIKKIKLTLGD 750

```

>dbj|BAD00915.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1279 bits (3310), Expect = 0.0, Method: Composition-based stats.
Identities = 651/750 (86%), Positives = 702/750 (93%), Gaps = 0/750 (0%)

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Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTKR+ R+A +NRKSPAENR+ VGK +SLL+V +FA+FLVNFAVIIG+G++FGTDL K 60
MKWTKRITRFAIRNRKSPAENRKIVGKYISLLAVVLFAVFLVNFAVIIGSGSKFGTDLVK

Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQ TRTPAKRGTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFN 120
EAKKVHQITRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFN 120

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEAYVKEQLSQPNLTQVSFGAKGNGITYANMMAIKKELETAEVKGIDF 180
KVAEVFHKYLDMEAYVKEQLSQPNLTQVSFGAKGNGITYANMMAIKKELETAEVKGIDF 180

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR 240
TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGKDGIIITYEKDR 240

Query 241 LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQ+T+DGKDVYTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGE 300
LGNIVPGTEQVSQQTVDGKDVYTTLSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGE 300

Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYEPGSTMKVMMMLAAIDNNTFPGGEVFN 360
Sbjct 301 ILATTQRPTF+ADTKEGITEDFVWRDILYQSNEYEPS KVMMLA++IDNNTFP GE FN 360
ILATTQRPTFNADTKEGITEDFVWRDILYQSNEYEPGSFAKVMMLASSIDNNTFPSGEYFN 360

Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSE KIADAT RDWDVNEGLT G MMTFSQGFHSSNVG +LLEQKMGDATWLDYL RFK 420
SSEFKIADATTRDWDVNEGLTTGGMMTFSQGFHSSNVGTSLEQKMGDATWLDYLNRFK 420

Query 421 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI 480
Sbjct 421 FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI 480
FGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFI 480

Query 481 SAIYDPNDQTARKSQKEIVGNPVSKEAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP 540
Sbjct 481 SAIYD N+Q+ RKSQKEIVGNPVSKEAAS TR +M+LVGTDP+YGTMYNH TGKP +TVP 540
SAIYDTNNQSVRKSQKEIVGNPVSKEAASLRTNMHMLVGTDPVYGTMYNHSTGKPTVTVP 540

Query 541 GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL 600
Sbjct 541 GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL 600
GQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENPDFILYVTVQQPEHYSGIQL 600

Query 601 GEFANPILERASAMKDSNLQTTAKALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQP 660
Sbjct 601 GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP 660
GEFATPILERASAMKESNLQSPAKNLKDVTTESYAMPSIKDISPGELAEALRRNLVQP 660

Query 661 IVVGTGTKIKNSSAEEGKNLAPNQVLLISDKAEVDPMYGWTKEAETLAKWLNIELEF 720
Sbjct 661 IVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PDYMGW KETAET AKWL+IELEF 720
IVVGTGTKIKETSVEEGTNLAPNQVLLLSDKVEEIPDYGWKKETAETFAKWLDIELEF 720

Query 721 QGSGSTVQKQDVRRNTAIKDIKITLTLGD 750
Sbjct 721 +GSGS VQKQDVR NTAIK+IKKI LTLGD 750
EGSGSVVQKQDVRRNTAIKNIKKIKLTLGD 750

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>dbj|BAD00940.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1275 bits (3300), Expect = 0.0, Method: Composition-based stats.
Identities = 647/750 (86%), Positives = 702/750 (93%), Gaps = 0/750 (0%)

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Query 1 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLSVFVFAIFLVNFAVIIGTGTRFGTDLAK 60
Sbjct 1 MKWTKR+ R+A +NRKSPAENR+ VGK +SLL+V +FA+FLVNFAVIIG+G++FGTDL K 60
MKWTKRITRFAIRNRKSPAENRKIVGKYISLLAVVLFAVFLVNFAVIIGSGSKFGTDLVK

Query 61 EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN 120
Sbjct 61 EAKKVHQ TRTPAKRGTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFN 120
EAKKVHQITRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFN 120

Query 121 KVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF 180
Sbjct 121 KVAEVFHKYLDMEAYVKEQLSQPNLTQVSFGAKGNGITYANMMAIKKDLKDVKEGIDF 180
KVAEVFHKYLDMEAYVKEQLSQPNLTQVSFGAKGNGITYANMMAIKKDLKDVKEGIDF 180

Query 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR 240
Sbjct 181 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR 240
TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGKDGIIITYEKDR 240

Query 241 LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGE 300
Sbjct 241 LGNIVPGTEQVSQ+T+DGKDVYTT+SSPLQSFME+QMDAFQEK+KGYMTATLVSAKTGE 300
LGNIVPGTEQVSQQTVDGKDVYTTLSSPLQSFMESQMDAFQEKLVKGYMTATLVSAKTGE 300

Query 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYEPGSTMKVMMMLAAIDNNTFPGGEVFN 360
Sbjct 301 ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYEPS MKVM LA++IDNNTFP GE FN 360
ILATTQRPTFDADTKEGITEDFVWRDILYQSNEYEPGSAMKVMTLASSIDNNTFPSGEYFN 360

Query 361 SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK 420
Sbjct 361 SSE KIADAT RDWDVNEGLT G MMTF QGFHSSNVGM+LLEQKMGDATWLDYL RFK 420
SSEFKIADATTRDWDVNEGLTTGGMMTFSQGFHSSNVG+LLEQKMGDATWLDYLNRFK 420

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Sbjct	361	SSEFKIADATTRDWDVNEGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRKFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKEAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Sbjct	481	SAIYD N+Q+ RKSQKEIVGNPVSKEAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVA+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLILSDKAEVPMYGTWKETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIK +S EEG NLAPNQVL+LSDK EE+PDYMGW KETAET AKWL+IELEF	720
Query	721	QGSSTVQKQDVRANTAIKDIKKITLTLGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLGD 750	

>gb|AA56845.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=666

Score = 1271 bits (3290), Expect = 0.0, Method: Composition-based stats.
Identities = 664/665 (99%), Positives = 664/665 (99%), Gaps = 0/665 (0%)

Query	82	RNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL	141
Sbjct	1	RNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL	60
Query	142	SQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLA	201
Sbjct	61	SQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLA	120
Query	202	QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV	261
Sbjct	121	QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV	180
Query	262	YTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGEILATTQRPTFDADTKEGITED	321
Sbjct	181	YTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGEILATTQRPTFDADTKEGITED	240
Query	322	FVWRDILYQSNEYEPGSTMTKVMMLAAAIIDNNTFPGGEVFNSSELKIADATIRDWDVNEGLT	381
Sbjct	241	FVWRDILYQSNEYEPGSTMTKVM LAAAIIDNNTFPGGEVFNSSELKIADATIRDWDVNEGLT	300
Query	382	GGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN	441
Sbjct	301	GGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN	360
Query	442	IVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGN	501
Sbjct	361	IVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGN	420
Query	502	PVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPVPGQNALKSGTAQIADEKNGGY	561
Sbjct	421	PVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPVPGQNALKSGTAQIADEKNGGY	480
Query	562	LVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ	621
Sbjct	481	LVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ	540
Query	622	TTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLA	681
Sbjct	541	TTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLA	600
Query	682	PNQQVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQGSSTVQKQDVRANTAIKDI	741
Sbjct	601	PNQQVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQGSSTVQKQDVRANTAIKDI	660
Query	742	KKITL 746	
Sbjct	661	KKITL 665	

>dbj|BAD00908.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
dbj|BAD00911.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=750

Score = 1269 bits (3283), Expect = 0.0, Method: Composition-based stats.
Identities = 643/750 (85%), Positives = 696/750 (92%), Gaps = 0/750 (0%)

Query	1	MKWTKRVIRYATKNRKSAPENRRRVGKSLSLLSVFVFAIFLVNFAVIIGTGRFGTDLAK	60
Sbjct	1	MKWT+++ R+A KNRKSPA+NRV VGK LS ++V +FA+FL NFA II G FGTDL K	60
Query	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Sbjct	61	EAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFN	120
Query	121	KVAEVFHKYLDMEESYVREQLSQPNLQVVSFGAKNGGITYANMMSIKKELEAAEVKGIDF	180
Sbjct	121	KVAEVFHKYLDMEAYVKEQLAQPNLTQVVSFGAKNGGITYANMMAIKNDLKTAGVEGIDF	180
Query	181	TTSPNRSYPNGQFASSFIGLAQLHENEDEGSKSLGTSGMESSLNSILAGTDGIITYEKDR	240
Sbjct	181	TTSPNRSYPNGQFASSFIGLAQLHENEDEG+K L+G+SG+ESSLNSILAGTDGIITYEKDR	240
Query	241	LGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE	300
Sbjct	241	LGNIVPGTEQ SQ T+DGKDVYTT+SSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGE	300
Query	301	ILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFN	360
Sbjct	301	ILATTQRPTF+ADTK+GIT+DFVWRDILYQSNYEPGS MKVM LA+AIDNNTFPGGE FN	360
Query	361	SSELKIADATIRDWDVNEGLTGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFK	420
Sbjct	361	SSELKIADATIRDWDVN+GLT G MMTFSQGFHSSNVGM+LLEQKMGDATWLDYLNRFK	420
Query	421	FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI	480
Sbjct	421	FGVPTRFGLTDEY GQLPADNIVNIA S+FGQGISVTQTQM+RAFTAIANDGVMLEPKFI	480
Query	481	SAIYDPNDQTARKSQKEIVGNPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTP	540
Sbjct	481	SAIYDPNDQ+ RKSQKEIVGNPVSK AAS TR +MV+VGTDPVYGTMYNHSTGKPVNP	540
Query	541	GQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQL	600
Sbjct	541	GQNVALKSGTAQIADEKNGGYL G T+YIFS VSM PAENPDFILYVTVQQPEHYSG+QL	600
Query	601	GEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQP	660
Sbjct	601	GEFANPILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQP	660
Query	661	IVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAEVPMYGWTKETAETLAKWLNIELEF	720
Sbjct	661	IVVGTGTKIK SS EEG NLAPNQVLL+LSDK EE+PDYMGW KETAET AKWL+IELEF	720
Query	721	QSGSSTVQKQDVRANTAIKDIKITLTLGD 750	
Sbjct	721	+GSGS VQKQDVR NTAIK+IKKI LTLGD 750	

>gb|ABB46504.1| penicillin binding protein 2x [Streptococcus pneumoniae]
gb|ABB46507.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=657

Score = 1258 bits (3254), Expect = 0.0, Method: Composition-based stats.
Identities = 656/657 (99%), Positives = 657/657 (100%), Gaps = 0/657 (0%)

Query	94	YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLQVVSFGA	153
Sbjct	1	YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLQVVSFGA	60
Query	154	KNGGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDEGSKSL	213
Sbjct	61	KNGGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDEGSKSL	120
Query	214	LGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPLQSF	273
Sbjct	121	LGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPLQSF	180
Query	274	ETQMDAFQEKVKGKMYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNY	333
Sbjct	181	ETQMDAFQEKVKGKMYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNY	240
Query	334	EPGSTMKVMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGFA	393
Sbjct	241	EPGSTMKVMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGFA	300
Query	394	HSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQG	453
Sbjct	301	HSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQG	360

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Query   454   ISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSFDAASLRT 513
Sbjct   361   ISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSFDAASLRT 420

Query   514   NMVLVGTDVPVGYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAV 573
Sbjct   421   NMVLVGTDVPVGYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAV 480

Query   574   SMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQ 633
Sbjct   481   SMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQ 540

Query   634   SPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQVVLILSDKA 693
Sbjct   541   SPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQVVLILSDKA 600

Query   694   EEVPDMPYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
Sbjct   601   EEVPDMPYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLGD 657

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>gb|AAN32862.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

Score = 1235 bits (3195), Expect = 0.0, Method: Composition-based stats.
Identities = 643/661 (97%), Positives = 652/661 (98%), Gaps = 0/661 (0%)

```

Query   90   DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV 149
Sbjct   1     DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV 60

Query   150  SFGAKGNGITIYANMMSIKKELEAAEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG 209
Sbjct   61   SFG+KGNGITIYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG 120

Query   210  SKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPL 269
Sbjct   121  SKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQQTVDGKDVYTTISSPL 180

Query   270  QSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPFTDADTKEGITEFVWRDILY 329
Sbjct   181  QSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPFTDADTKEGIT+DFVWRDILY 240

Query   330  QSNYEPGSTMKVMMMLAAIDNNTFPGGEVFNSELKIADATIRDWDVNEGLTGGRMMTFS 389
Sbjct   241  QSNYEPGSAMKVMTLAAIDNNTFPGGEVFNSELKVADVTTRDWDVNEGLTGGMMTFS 300

Query   390  QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS 449
Sbjct   301  QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS 360

Query   450  FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSFDAAS 509
Sbjct   361  FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKE+VGNPVSFDAAS 420

Query   510  LTRTNMVLVGTDVPVGYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYI 569
Sbjct   421  LTRTHMVLVGTDVPVGYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTNYI 480

Query   570  FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ 629
Sbjct   481  FSAVSMNPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ 540

Query   630  VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQVVLIL 689
Sbjct   541  VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQVVLIL 600

Query   690  SDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLG 749
Sbjct   601  SDKAEVPMYGTWKATAETFAKWLNIIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLG 660

Query   750  D 750
Sbjct   661  D 661

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>gb|AAN32857.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
>gb|AAN32858.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

Score = 1234 bits (3194), Expect = 0.0, Method: Composition-based stats.
Identities = 643/661 (97%), Positives = 653/661 (98%), Gaps = 0/661 (0%)

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Query   90   DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV 149
          DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV

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Sbjct	1	DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV	60
Query	150	SFGAKNGITYANMMSIKKELEAAEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG	209
Sbjct	61	SFGAKNGITYANMMSIKKELEAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG	120
Query	210	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPL	269
Sbjct	121	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQ+SQ+T+DGKDVYTTISSPL	180
Query	270	QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY	329
Sbjct	181	QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGIT+DFVWRDILY	240
Query	330	QSNYEPGSTMKVMMMLAAAI DNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFS	389
Sbjct	241	QSNYEPGS MKVM LAA+IDNNTFPGGE FNSSELKIAD TIRDWDVNEGLTGG MMTFS	300
Query	390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct	301	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	360
Query	450	FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAAS	509
Sbjct	361	FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAAS	420
Query	510	LTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYI	569
Sbjct	421	LTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLT+YI	480
Query	570	FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ	629
Sbjct	481	FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAK+LEQ	540
Query	630	VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVVLIL	689
Sbjct	541	VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVVLIL	600
Query	690	SDKAEVDPDYGWTKETAETLAKWLNIELEFQSGSGTVQKQDVRANTAIKDIKKITLTLG	749
Sbjct	601	SDKAEVDPDYGWTK TAET AKWLNIELEF+GSG+TVQKQDVRANTAIKDIKKITLTLG	660
Query	750	D 750	
Sbjct	661	D 661	

>emb|CAB65447.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1230 bits (3182), Expect = 0.0; Method: Composition-based stats.
Identities = 639/666 (95%), Positives = 653/666 (98%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFSGAKNGITYANMMSIKKELEAAEVKGI DFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFSGAKNGITYANMMSIKKELEAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW	324
Sbjct	181	ISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW	240
Query	325	RDILYQSNYEPGSTMKVMMMLAAAI DNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGR	384
Sbjct	241	RDILYQSNYEPGSTMKVMMMLAAAI DNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGR	300
Query	385	MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	360
Query	445	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504
Sbjct	361	IA S+FGQGISVTQTQM+RAFTAIANDGVMLEPKFISA+YDPNDQ+ RKSQKEIVGNPVS	420
Query	505	KDAASLTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG	564
Sbjct	421	KEAASVTRDHMMVMVGTDPTYGTMYNHSTGKATVNVPGQNVALKSGTAEIADEKNGGYLTG	480
Query	565	LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA	624

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-   T+ IFS VSM PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQTTA
Sbjct 481 STNNIFSVSMHPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNLQTTA 540

Query 625 KALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQ 684
-   KALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQ
Sbjct 541 KALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQ 600

Query 685 QVLILSDKAAEVPDMYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKI 744
-   QVLILSDKAAEVPDMYGWTKETAET AKWLNIELEF+GSGSTVQKQDVRANTAIKDIKKI
Sbjct 601 QVLILSDKAAEVPDMYGWTKETAETFAKWLNIELEFEGSGSTVQKQDVRANTAIKDIKKI 660

Query 745 TLTLGD 750
-   TLTLGD
Sbjct 661 TLTLGD 666

```

>gb|AAN32865.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

Score = 1222 bits (3161), Expect = 0.0, Method: Composition-based stats.
Identities = 636/661 (96%), Positives = 651/661 (98%), Gaps = 0/661 (0%)

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Query 90 DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV 149
Sbjct 1 DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV 60

Query 150 SFGAKGNGITYANMMSIKKELEAAEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG 209
-   SFGAKGNGITYANMMSIKKELEAAEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG
Sbjct 61 SFGAKGNGITYANMMSIKKELEAAEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG 120

Query 210 SKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPL 269
-   SKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPL
Sbjct 121 SKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPL 180

Query 270 QSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY 329
-   QSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGIT+DFVWRDILY
Sbjct 181 QSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITKDFVWRDILY 240

Query 330 QSNYEPGSTMKVMMLAAAI DNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFS 389
-   QSNYEPGSTMKVMMLAAAI DNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGG MMTFS
Sbjct 241 QSNYEPGSTMKVMMLAAAI DNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGM TFS 300

Query 390 QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS 449
-   QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS
Sbjct 301 QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS 360

Query 450 FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAAS 509
-   FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKE+VGNPVS KDAAS
Sbjct 361 FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEVGNPVS KDAAS 420

Query 510 LTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYI 569
-   LTRTNM+LVGTDPVYGTMYNHSTGKPTV VPGQNVALKSGTA+IADEKNGGYLVG T+ I
Sbjct 421 LTRTNMILVGTDPVYGTMYNHSTGKPTVNVPGQNVALKSGTAEIADEKNGGYLVGSTNNI 480

Query 570 FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ 629
-   FS V+M+PAE+PDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ AK L++
Sbjct 481 FSVVAMNPAEDPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNLQSPAKNLDK 540

Query 630 VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQVVLIL 689
-   V+ +S Y MPS+KDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQVVLIL
Sbjct 541 VTTESSYAMPSIKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQVVLIL 600

Query 690 SDKAAEVPDMYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLG 749
-   SDKAAEVPDMYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLG
Sbjct 601 SDKAAEVPDMYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLG 660

Query 750 D 750
-   D
Sbjct 661 D 661

```

>emb|CAD90770.1| penicillin-binding protein 2x [Streptococcus pneumoniae]
Length=702

Score = 1217 bits (3150), Expect = 0.0, Method: Composition-based stats.
Identities = 627/702 (89%), Positives = 665/702 (94%), Gaps = 0/702 (0%)

```

Query 49 GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT 108
Sbjct 1 GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT 60

Query 109 GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVVSFGAKGNGITYANMMSIKK 168
-   GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVVSFG+KNGITYANMMSIKK
Sbjct 61 GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVVSFGSKGNGITYANMMSIKK 120

Query 169 ELEAAEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA 228

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-   Sbjct  121  ELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA 180
      ELETAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA

-   Query  229  GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKY 288
      GTDGIITYEKDR+GNIVPGTE VSQ+T+DGKDVTYTT+SSPLQSFMETQMDAF EKVKGKY
-   Sbjct  181  GTDGIITYEKDRVGNIVPGTELVSQQTVDGKDVTYTTLSPLQSFMETQMDAFLEKVKGKY 240

      Query  289  MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI 348
      MTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++I
-   Sbjct  241  MTATLVSAKTGEILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSI 300

      Query  349  DNNTFPGGEVFNSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMG 408
      DNNTFP GE FNSSE KIADAT RDWDVN+GLT G MMTF QGFAHSSNVGM+LLEQKMG
-   Sbjct  301  DNNTFPSGEYFNSSEFKIADATT RDWDVNDGLTTGGMMTFLQGFAHSSNVGMSLLEQKMG 360

      Query  409  DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAI 468
      DATWLDYL RKFQGVPTFRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAI
-   Sbjct  361  DATWLDYLRKFQGVPTFRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAI 420

      Query  469  ANDGVMLEPKFISAIYDPNDQTARKSKEIVGNPVSCKDAASLTRTNMVLVGTDPVYGTMY 528
      ANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVSCK+AAS TR +M+LVGTDP+YGTMY
-   Sbjct  421  ANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRNHMILVGTDPVYGTMY 480

      Query  529  NHSTGKPTVTVPQGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT 588
      NH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVT
-   Sbjct  481  NHYTGKPIITVPQGQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENPDFILYVT 540

      Query  589  VQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYMPSPVKDISPGD 648
      VQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+
-   Sbjct  541  VQQPEHYSGIQLGEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGE 600

      Query  649  LAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQQVLILSDKAEVPMYGTWKETAE 708
      LAE LRRN+VQPIVVGTGTKIK +S EEG NLAPNQQVL+LSDK EE+PMYGW KETAE
-   Sbjct  601  LAEALRRNIVQPIVVGTGTKIKETSVEEGTNLAPNQQVLLLSDKVEEIPMYGWKKETAE 660

      Query  709  TLAKWLNIELEFQGSSTVQKQDVRANTAIAIKDIKITLTLGD 750
      T AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI LTLGD
-   Sbjct  661  TFAKWLDIELEFEGSGSVVQKQDVRTNTAIAIKIKIKLTLGD 702

```

>emb|CAD90771.2| penicillin-binding protein 2x [Streptococcus pneumoniae]
Length=702

Score = 1209 bits (3129), Expect = 0.0, Method: Composition-based stats.
Identities = 622/702 (88%), Positives = 662/702 (94%), Gaps = 0/702 (0%)

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Query  49  GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT 108
      GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT
-   Sbjct  1  GTGTRFGTDLAKEAKKVHQTTTRTPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSAT 60

      Query  109  GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKK 168
      GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMM+IKK
-   Sbjct  61  GKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMAIKK 120

      Query  169  ELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA 228
      +L+ A V+GIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA
-   Sbjct  121  DLKDAVSEGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILA 180

      Query  229  GTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKY 288
      G DGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVTYTT+SSPLQSFMETQMDAF EKVKGKY
-   Sbjct  181  GKDGIITYEKDRLGNIVPGTEQVSQQTVDGKDVTYTTLSPLQSFMETQMDAFLEKVKGKY 240

      Query  289  MTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMMLAAAI 348
      MTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVWRDILYQSNYEPGS KVMMLA++I
-   Sbjct  241  MTATLVSAKTGEILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSFAKVMMLASSI 300

      Query  349  DNNTFPGGEVFNSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMG 408
      DNNTFP GE FNSSE KIADAT RDWDVN GLT G MMTF QGFAHSSNVG +LLEQKMG
-   Sbjct  301  DNNTFPSGEYFNSSEFKIADATT RDWDVNAGLTTGGMMTFLQGFAHSSNVGTSLLEQKMG 360

      Query  409  DATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAI 468
      DATWLDYL RKFQGVPTFRFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAI
-   Sbjct  361  DATWLDYLRKFQGVPTFRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAI 420

      Query  469  ANDGVMLEPKFISAIYDPNDQTARKSKEIVGNPVSCKDAASLTRTNMVLVGTDPVYGTMY 528
      ANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVSCK+AAS TR +M+LVGTDP+YGTMY
-   Sbjct  421  ANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRNHMILVGTDPVYGTMY 480

      Query  529  NHSTGKPTVTVPQGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVT 588
      NH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG T+YIFS V+M+PAENPDFILYVT
-   Sbjct  481  NHYTGKPIITVPQGQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVVTMNPENPDFILYVT 540

      Query  589  VQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQSPYMPSPVKDISPGD 648
      VQQPEH+SGIQLGEFA PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+
-   Sbjct  541  VQQPEHFSGIQLGEFATPILERASAMKESLNLQSPAKNLDKVTTESSYAMPSIKDISPGE 600

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- Query 649 LAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKAAEEVPDMYGWTKETAE 708
  Sbjct 601 LAE LRRN+VQPIVVGTGTKIK +S EEG NLAPNQVLL+LSDK EE+PDMYGW KETAE 660
  LAEALRRNIVQPIVVGTGTKIKETSVEEGTNLAPNQVLLILSDKVEEIPDMYGWKKETAE

- Query 709 TLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLGD 750
  Sbjct 661 T AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI LTLGD 702
  TFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNIKKIKLTLGD

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>gb|AA556843.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 gb|AA556844.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 Length=669

Score = 1207 bits (3122), Expect = 0.0, Method: Composition-based stats.
 Identities = 625/669 (93%), Positives = 648/669 (96%), Gaps = 0/669 (0%)

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Query 82  RNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL 141
Sbjct 1  RNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL 60

Query 142 SQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLA 201
Sbjct 61 SQPNLKQVSFG+KNGGITYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLA 120
SQPNLKQVSFGSKGNGITYANMMSIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIGLA

Query 202 QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV 261
Sbjct 121 QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDV 180
QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDV

Query 262 YTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITED 321
Sbjct 181 YTTISSPLQSFMETQMDAF +KVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITED 240
YTTISSPLQSFMETQMDAF LQKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITED

Query 322 FVWRDILYQSNEYEPGSTMKVMMLAAAI DNNTFPGGEVFNSSELKIADATIRDWDVNEGLT 381
Sbjct 241 FVWRDILYQSNEYEPGS +KVM LA++IDNNTFP GE FNSSE KIAD T RDWDVN+GLT 300
FVWRDILYQSNEYEPGSALKVMTLASSIDNNTFPSGEYFNSSEFKIADVTRDWDVNDGLT

Query 382 GGRMMTFSQGFAHSSNVGMTLLEQKMGDWTLDYLNRFKFGVPTRFGLTDEYAGQLPADN 441
Sbjct 301 G MMTF QGFAHSSNVGM+LLEQKMGDWTLDYLNRFKFGVPTRFGLTDEYAGQLPADN 360
TGGMMTFLQGFAHSSNVGMSLLEQKMGDWTLDYLNRFKFGVPTRFGLTDEYAGQLPADN

Query 442 IVNIAQSSFGQGISVTQTQMIRAF TA IANDGVMLEPKFISAIYDPNDQTARKSQKEIVGN 501
Sbjct 361 IVNIAQSSFGQGISVTQTQM+RA TAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVG 420
IVNIAQSSFGQGISVTQTQMLRALTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGK

Query 502 PVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGY 561
Sbjct 421 PVS+DAASLRTNM+LVGTDP+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGY 480
PVSEDAASLRTNMILVGTDP IYGTMYNHYTGKPIITVPQONVAVKSGTAQIADEKNGGY

Query 562 LVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ 621
Sbjct 481 LVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ 540
LVGSTNYIFSVVTMNPANPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQ

Query 622 TTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLA 681
Sbjct 541 TTAKALEQVS+QSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLA 600
TTAKALEQVSKQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLA

Query 682 PNQQVLLILSDKAAEEVPDMYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDI 741
Sbjct 601 PNQQVLLILSDKAAEEVPDMYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDI 660
PNQQVLLILSDKAAEEVPDMYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDI

Query 742 KKITLTLGD 750
Sbjct 661 KKITLTLGD 669

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>gb|AA556850.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 Length=670

Score = 1206 bits (3119), Expect = 0.0, Method: Composition-based stats.
 Identities = 627/670 (93%), Positives = 647/670 (96%), Gaps = 0/670 (0%)

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Query 81  DRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ 140
Sbjct 1  DRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ 60
DRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ

Query 141 LSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGL 200
Sbjct 61 LSQPNLKQVSFGAKGNGITYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGL 120
LSQPNLKQVSFGAKGNGITYANMMSIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIGL

Query 201 AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKD 260
Sbjct 121 AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKD 180
AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKD

Query 261 VYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITE 320
Sbjct 181 VYTTISS LQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITE 240
VYTTISS TLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITE

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Query 321 DFVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFP GGGEVFNSSSELKIADATIRDWDVNEGL 380
Sbjct 241 DFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GL 300

Query 381 TGGRRMTFSQGF AHS SNVGMTLLEQKMGD ATWLDYLNRFKFGVPTRFGLTDEYAGQLPAD 440
Sbjct 301 TGGMMTFLQGFAHSSNVGMSLLEQKMGD ATWLDYLKRKFGVPTRFGLTDEYAGQLPAD 360

Query 441 NIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKS QKEIVG 500
Sbjct 361 NIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKS QKEIVG 420

Query 501 NPVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGG 560
Sbjct 421 NPVSKEAASSTRNHMILVGTDPVYGTMYNHSTGKPTVTVPQGNVAVKSGTAQIADEKNGG 480

Query 561 YLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNL 620
Sbjct 481 YLVGSTNYIFSVVTMNPENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKDSLNL 540

Query 621 QTTAKALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNL 680
Sbjct 541 QTTAKALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNL 600

Query 681 APNQQVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKD 740
Sbjct 601 APNQQVLILSDKVEEVPDMPYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKD 660

Query 741 IKKITLTLGD 750
Sbjct 661 IKKITLTLGD 670

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>gb|AA556847.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=669

Score = 1204 bits (3114), Expect = 0.0, Method: Composition-based stats.
Identities = 621/669 (92%), Positives = 644/669 (96%), Gaps = 0/669 (0%)

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Query 82 RNVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL 141
Sbjct 1 RNVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL 60

Query 142 SQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLA 201
Sbjct 61 SQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLA 120

Query 202 QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV 261
Sbjct 121 QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV 180

Query 262 YTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITED 321
Sbjct 181 YTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITED 240

Query 322 FVWRDILYQSNYEPGSTMKVMMMLAAAI DNNTFP GGGEVFNSSSELKIADATIRDWDVNEGLT 381
Sbjct 241 FVWRDILYQSNYEPGSTMKVM LAAAI DNNTFP GGGEVFNSSSELKIADATIRDWDVNEGLT 300

Query 382 GGRMMTFSQGF AHS SNVGMTLLEQKMGD ATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN 441
Sbjct 301 GGRMMTFSQGF AHS SNVGMTLLEQKMGD ATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN 360

Query 442 IVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKS QKEIVGN 501
Sbjct 361 IVNIA S+FGQGISVTQTQM+RAFTAIANDGVMLEPKFISA+YDPNDQ+ RKSQKE+VGN 420
IVNIA SFAFGQGISVTQTQMLRAFTAIANDGVMLEPKFISALYDPNDQSVRKS QKEVVGN

Query 502 PVS KDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGGY 561
Sbjct 421 PVSKEAASVTRDQMVMVGTDPYGTMYNHSTGKATVNVPGQGNVALKSGTAEIADEKNGGY 480

Query 562 LVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ 621
Sbjct 481 LVGSTNNIFSVVAMNPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ 540

Query 622 TTAKALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLA 681
Sbjct 541 SPAKNLDQVTTESYAMPSIKDISPGDLAEALRRNIVQPIVVGTGTGIKESSVEEGKNLA 600

Query 682 PNQQVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDI 741
Sbjct 601 PNQQVLLLSDKVEEIPDMPYGWKETAETFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNI 660

Query 742 KKITLTLGD 750
Sbjct KKI LTLGD

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• Sbjct 661 KKIKLTLGD 669

>gb|AA556846.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=670

Score = 1198 bits (3099), Expect = 0.0, Method: Composition-based stats.
Identities = 621/670 (92%), Positives = 647/670 (96%), Gaps = 0/670 (0%)

Query	81	DRNGVPVIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ	140
Sbjct	1	DRNGVPVIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ	60
Query	141	LSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKIGIDFTTSPNRSYPNGQFASSFIGL	200
Sbjct	61	LSQPNLKQVSFGAKGNGITYANMMAIKKELETAEVKIGIDFTTSPNRSYPNGQFASSFIGL	120
Query	201	AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKD	260
Sbjct	121	AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQ+T+DGKD	180
Query	261	VYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITE	320
Sbjct	181	VYTTISS LQSFMETQ+AFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEG+T+	240
Query	321	DFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWVDNEGL	380
Sbjct	241	DFVWRDILYQSNYEPGSTMKVM LAAIDNNTFPGGEVFNSSSELK+AD TIRDWVDNEGL	300
Query	381	TGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTREFGLTDEYAGQLPAD	440
Sbjct	301	TGG MMTFSQGF SSVNGMTLLEQKMGDATWLDYLNRFKFGVPTREFGLTDEYAGQLPAD	360
Query	441	NIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVG	500
Sbjct	361	NIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISALYDPNDQSVRKSQKEIVG	420
Query	501	NPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGG	560
Sbjct	421	NPVSK+AAS+TR +MV+VGTD YGTMYNHSTGKPTVTVPQGNVALKSGTA+IADEKNGG	480
Query	561	YLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNL	620
Sbjct	481	YLVG T+YIFSAVSM+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNL	540
Query	621	QTTAKALEQVSQQSPYPMPVSKDISPGDLAEELRRNLVQPIVVGTGKTIKNSSAEEGKNL	680
Sbjct	541	Q+TAK LEQ S+ + Y MP+ KD +PGDLAEELRRNLVQPIVVGTGKTIK +S EEG NL	600
Query	681	APNQOVLILSDKAEEVPDYGWTKETAETLAKWLNIELEFGSGSTVQKQDVRANTAIKD	740
Sbjct	601	APNQOVL+LSDK EE+PDYGW KETAET AKWLNIELEF+GSGSTVQKQDVRANTAIKD	660
Query	741	IKKITLTLGD 750	
Sbjct	661	IKKITLTLGD 670	

>gb|AA556857.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=666

Score = 1197 bits (3096), Expect = 0.0, Method: Composition-based stats.
Identities = 623/666 (93%), Positives = 643/666 (96%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNGITYANMMSIKKELETAEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW	324
Sbjct	181	ISS LQSFMETQMDAF EKVKGYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVW	240
Query	325	RDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWVDNEGLTGGR	384
Sbjct	241	RDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT G	300
Query	385	MMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTREFGLTDEYAGQLPADNIVN	444
		MMTF QGFHSSNVGM+LLEQKMGDATWLDYL RKFVPTREFGLTDEYAGQLPADNIV+	

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* Sbjct 301 MMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFKFGVPTRFGLTDEYAGQLPADNIVS 360
Query 445 IAQSSFGQGIGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS 504
IAQSSFGQGIGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVS
* Sbjct 361 IAQSSFGQGIGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVS 420
Query 505 KDAASLRTNMLVLTGDPVYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGGYLVG 564
K+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVPGQNV+A+KSGTAQIADEKNGGYLVG
Sbjct 421 KEAASLRTNMLVLTGDPVYGTMYNHSTGKPTVTVPQGNVAVKSGTAQIADEKNGGYLVG 480
Query 565 LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA 624
T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMKDSLNLQTTA
Sbjct 481 STNYIFSVVMTMNAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKDSLNLQTTA 540
Query 625 KALEQVSQQSPYPMPVSVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQ 684
KALEQVSQQSPYPMPVSVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQ
Sbjct 541 KALEQVSQQSPYPMPVSVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQ 600
Query 685 QVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKI 744
QVLILSDK EEVPMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKI
Sbjct 601 QVLILSDKVEEVPDMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKI 660
Query 745 TLTLGD 750
Sbjct 661 TLTLGD 666

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>emb|CAB65444.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1188 bits (3073), Expect = 0.0, Method: Composition-based stats.
Identities = 612/666 (91%), Positives = 640/666 (96%), Gaps = 0/666 (0%)

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Query 85 VPAAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP 144
Sbjct 1 VPAAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP 60
Query 145 NLKQVSFGAKNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLAQLH 204
NLKQVSFGAKNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLAQLH
Sbjct 61 NLKQVSFGAKNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLAQLH 120
Query 205 ENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT 264
ENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTT
Sbjct 121 ENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDVYTT 180
Query 265 ISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEFVW 324
+SSPLQSFMETQMDAF +KVKGYMTATLVSAKTGEILATTQRPTF+ADTKEGITEFVW
Sbjct 181 LSSPLQSFMETQMDAFLQKVKGYMTATLVSAKTGEILATTQRPTFNADTKEGITEFVW 240
Query 325 RDILYQSNYEPGSTMKVMMLA A AIDNNTFPGGEVFNSELKIADATIRDWDVNEGLTGGR 384
RDILYQSNYEPGS MKVM L A A AIDNNTFPGGE FNSSELKIAD TIRDWDVN+GLT GR
Sbjct 241 RDILYQSNYEPGSAMKVMTL A A AIDNNTFPGGEYFNSELKIADV TIRDWDVNDGLTTGR 300
Query 385 MMTFSQGF A HSSNVGMSLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN 444
MMTF QGFA SSVNGM+LLEQKMGD TWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN
Sbjct 301 MMTFLQGFALSSNVGMSLLEQKMGDPWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN 360
Query 445 IAQSSFGQGIGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS 504
IAQSSFGQGIGISVTQTQMIRAFTAIANDGVMLEPKFI+A+YDPNDQT RKSQKEIVGNPVS
Sbjct 361 IAQSSFGQGIGISVTQTQMIRAFTAIANDGVMLEPKFITALYDPNDQTVRKSQKEIVGNPVS 420
Query 505 KDAASLRTNMLVLTGDPVYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGGYLVG 564
KDAASLRTNM+LVGTDPVYGTMYNHSTGKPTVTVPQGNVALKSGTA+IADEKNGGYLVG
Sbjct 421 KDAASLRTNMILVLTGDPVYGTMYNHSTGKPTVTVPQGNVALKSGTAETIADEKNGGYLVG 480
Query 565 LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA 624
T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ A
Sbjct 481 STNYIFSVVAMNPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNLQSPA 540
Query 625 KALEQVSQQSPYPMPVSVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAPNQ 684
K L+QV+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTGIK +S EEGKNLAPNQ
Sbjct 541 KNLDQVTTESSYAMPSIKDISPGELAE LRRNIVQPIVVGTGTGIKETSVEEGKNLAPNQ 600
Query 685 QVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKI 744
QVL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI
Sbjct 601 QVLLLSDKVEEIPDMYGWKKETAETFAKWLDIELEFEGSGSIVQKQDVRTNTAIKNIKKI 660
Query 745 TLTLGD 750
Sbjct 661 KLT LGD 666

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>gb|AAN32852.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 gb|AAN32853.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 gb|AAN32854.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
 Length=661

Score = 1187 bits (3071), Expect = 0.0, Method: Composition-based stats.
Identities = 618/661 (93%), Positives = 638/661 (96%), Gaps = 0/661 (0%)

Query	90	DATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV	149
Sbjct	1	DATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV	60
Query	150	SFGAKGNGITAYANMMSIKKELEAAEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG	209
Sbjct	61	SFGAKGNGITAYANMMSIKKELE AEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG	120
Query	210	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPL	269
Sbjct	121	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTTISS L	180
Query	270	QSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY	329
Sbjct	181	QSFMETQMDAF EKVKGKGYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVWRDILY	240
Query	330	QSNYEPGSTMKVMMLAAAI DNNTFP GGEVFNSSSELKIADATIRDWVDVNEGLTGGRMMTFS	389
Sbjct	241	QSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT G MMTF	300
Query	390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct	301	QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSS	360
Query	450	FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAAS	509
Sbjct	361	FGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVS K+AAS	420
Query	510	LTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYI	569
Sbjct	421	TR +M+LVGTD+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG T+YI	480
Query	570	FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ	629
Sbjct	481	FS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMKDSLNLQTTAKALEQ	540
Query	630	VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGVTGTKIKNSSAEEGKNLAPNQVVLIL	689
Sbjct	541	VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGVTGTKIKNSSAEEGKNLAPNQVVLIL	600
Query	690	SDKAEVDPDMPYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDV RANTAIKDIIKITLTG	749
Sbjct	601	SDK EEVDPDMPYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDV RANTAIKDIIKITLTG	660
Query	750	D 750	
Sbjct	661	D 661	

>gb|AAN32861.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

Score = 1186 bits (3069), Expect = 0.0, Method: Composition-based stats.
Identities = 614/661 (92%), Positives = 635/661 (96%), Gaps = 0/661 (0%)

Query	90	DATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV	149
Sbjct	1	DATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV	60
Query	150	SFGAKGNGITAYANMMSIKKELEAAEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG	209
Sbjct	61	SFGAKGNGITAYANMMSIKKELE AEVKGI DFTTSPNRSYPNGQFASSFIGLAQLHENEDG	120
Query	210	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPL	269
Sbjct	121	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTTISS L	180
Query	270	QSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY	329
Sbjct	181	QSFMETQMDAFQEKVKGYMTAALVSAKTGEILATTQRPTFDADTKEGLTKDFVWRDILY	240
Query	330	QSNYEPGSTMKVMMLAAAI DNNTFP GGEVFNSSSELKIADATIRDWVDVNEGLTGGRMMTFS	389
Sbjct	241	QSNYEPGS MKVM LAAAI DNNTFP GGEVFNSSSELK+AD TIRDWVDVNEGLTG MMTFS	300
Query	390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct	301	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	360
Query	450	FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAAS	509
Sbjct	361	FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTVRKSQKEIVGNPVS KDAAS	420

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Query   510  LTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYI  569
Sbjct   421  QTRTHMVLVGTDVPVYGTMMHNSHGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGTTDYI  480

Query   570  FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ  629
Sbjct   481  FSAVSM+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERA AMKDSLNLQ+TAK L+Q  540
FSAVSMNPAENPDFILYVTVQQPEHYSGIQLGEFANPILERAVAMKDSLNLQSTAKTLDQ

Query   630  VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQOVLIL  689
Sbjct   541  VTNQSAYAMPSIKDISPGDLAEALRRNIVQPIVVGTGTKIKESSVEEGTNLAPNQOVLILL  600

Query   690  SDKAEVVPDMPYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTG  749
Sbjct   601  SDK EE+PDMPYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI LTG  660
SDKVEEIPDMPYGWKKETAETFAKWL DIELEFEGSGSVVQKQDVRTNTAIKNIKKIKLTG

Query   750  D      750
Sbjct   661  D      661

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>gb|AAN32863.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

Score = 1183 bits (3061), Expect = 0.0, Method: Composition-based stats.
Identities = 611/661 (92%), Positives = 639/661 (96%), Gaps = 0/661 (0%)

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Query   90  DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV  149
Sbjct   1  DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV  60

Query   150  SFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG  209
Sbjct   61  SFG+KNGNGITYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG  120
SFGSKGNGITYANMMSIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG

Query   210  SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPL  269
Sbjct   121  SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTTISSPL  180
SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDVYTTISSPL

Query   270  QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY  329
Sbjct   181  QSFMETQ+AFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEG+T+DFVWRDILY  240
QSFMETQ+AFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY

Query   330  QSNYEPGSTMKVMLAAAI DNNTFPGGEVFNSELKIADATIRDWDVNEGLTGGRMMTFS  389
Sbjct   241  QSNYEPGSTMKVMTLAAAI DNNTFPGGEVFNSELKIADV TIRDWDVNDGLTTGRMMTFL  300

Query   390  QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS  449
Sbjct   301  QGFALSSNVGMSLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS  360

Query   450  FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAAS  509
Sbjct   361  FGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEVVGNPVS KDAAS  420

Query   510  LTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYI  569
Sbjct   421  LTRTNM+LVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLT+YI  480
LTRTNMILVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTNYI


Query   570  FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ  629
Sbjct   481  FSAVSM+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ AK L++  540
FSAVSMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQSPAKNLDK


Query   630  VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQOVLIL  689
Sbjct   541  VTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGTNLAPNQOVLILL  600


Query   690  SDKAEVVPDMPYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTG  749
Sbjct   601  SDK EE+PDMPYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI LTG  660
SDKVEEIPDMPYGWKKETAETFAKWL DIELEFEGSGSVVQKQDVRTNTAIKNIKKIKLTG

Query   750  D      750
Sbjct   661  D      661

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>pdb|1K25|A  Chain A, Pbp2x From A Highly Penicillin-Resistant Streptococcus Pneumoniae Clinical Isolate

>pdb|1K25|B  Chain B, Pbp2x From A Highly Penicillin-Resistant Streptococcus Pneumoniae Clinical Isolate

>pdb|1K25|C  Chain C, Pbp2x From A Highly Penicillin-Resistant Streptococcus Pneumoniae Clinical Isolate

pdb|1K25|D Chain D, Pbp2x From A Highly Penicillin-Resistant Streptococcus
Pneumoniae Clinical Isolate
Length=685

Score = 1183 bits (3060), Expect = 0.0, Method: Composition-based stats.
Identities = 607/685 (88%), Positives = 646/685 (94%), Gaps = 0/685 (0%)

Query	66	HQTRTRVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEV	125
Sbjct	1	HQ TRTVP AKRGTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFNKVAEV	60
Query	126	FHKYLDMEESYVREQLSQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDFTTSPN	185
Sbjct	61	FHKYLDMEESYVREQLSQPNLKQVSFG+KNGITYANMM+IKKELE AEVKGIDFTTSPN	120
Query	186	RSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIV	245
Sbjct	121	RSYPNGQFASSFIGLAQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDR+GNIV	180
Query	246	PGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKMYMTATLVSAKTGEILATT	305
Sbjct	181	PGTE VSQ+T+DGKDVYTT+SSPLQSFMETQMDAF EKVKGKMYMTATLVSAKTGEILATT	240
Query	306	QRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAI DNNTFP GG EVFNSSELK	365
Sbjct	241	QRPTFNADTKEGITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSELK	300
Query	366	IADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPT	425
Sbjct	301	IADAT RDWDVNEGLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPT	360
Query	426	RFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYD	485
Sbjct	361	RFGLTDEYAGQLPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD	420
Query	486	PNDQTARKSKEIVGNPVSKEAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPGQNV	545
Sbjct	421	N+Q+ RKSQKEIVGNPVSKEAAS TR +M+LVGTDP+YGTMYNH TGKP +TVPGQNV	480
Query	546	LKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFAN	605
Sbjct	481	+KSGTAQIADEKNGGYLVG T+YIFSAV+M+PAENPDFILYVTVQQPEHYSGIQLGEFA	540
Query	606	PILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVGT	665
Sbjct	541	PILERASAMK+SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVGT	600
Query	666	GTKIKNSSAEEGKNLAPNQVLLISDKAEEVPDMYGWTKETAETLAKWLNIELEFQSGSGS	725
Sbjct	601	GTKIK +S EEG NLAPNQVLL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS	660
Query	726	TVQKQDVRANTAIDIKKITLTLGD	750
Sbjct	661	VQKQDVR NTAIK+IKKI LTLGD	685

>gb|ABB46505.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=657

Score = 1182 bits (3059), Expect = 0.0, Method: Composition-based stats.
Identities = 614/657 (93%), Positives = 635/657 (96%), Gaps = 0/657 (0%)

Query	94	YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGA	153
Sbjct	1	YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGA	60
Query	154	KNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSL	213
Sbjct	61	KNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSL	120
Query	214	LGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSF	273
Sbjct	121	LGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTTISS LQSF	180
Query	274	ETQMDAFQEKVKGKMYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNY	333
Sbjct	181	ETQMDAF EKVKGKMYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVWRDILYQSNY	240
Query	334	EPGSTMKVMMLAAAI DNNTFP GG EVFNSSELKIADATIRDWDVNEGLTGGRMMTFSQGFA	393
Sbjct	241	EPGS MKVM LA+++DNNTFP GE FNSSE KIADAT RDWDVN+GLT G MMTF QGFA	300
Query	394	HSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQG	453
Sbjct	301	HSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQG	360

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Query   454   ISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSFDAASLTRT   513
Sbjct   361   ISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRN   420

Query   514   NMVLVGTDVPYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAV   573
        +M+LVGTDP+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG T+YIFS V
Sbjct   421   HMILVGTDPLYGTMYNHSTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVV   480

Query   574   SMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQ   633
        +M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMKDSLNLQTTAKALEQVSQQ
Sbjct   481   TMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKDSLNLQTTAKALEQVSQQ   540

Query   634   SPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKA   693
        SPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLILSDK
Sbjct   541   SPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKV   600

Query   694   EEVPDAMYGWTKEATAETLAKWLNIELEFQSGSGSTVQKQDVRRANTAIKDIKKITLTLGD   750
        EEVPDAMYGWTKEATAETLAKWLNIELEFQSGSGSTVQKQDVRRANTAIKDIKKITLTLGD
Sbjct   601   EEVPDAMYGWTKEATAETLAKWLNIELEFQSGSGSTVQKQDVRRANTAIKDIKKITLTLGD   657

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>gb|ABB46506.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=657

Score = 1181 bits (3055), Expect = 0.0, Method: Composition-based stats.
Identities = 614/657 (93%), Positives = 634/657 (96%), Gaps = 0/657 (0%)

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Query   94    YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGA   153
Sbjct   1      YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGA   60

Query   154   KNGGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDEGSKSL   213
        KNGGITYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDEGSKSL
Sbjct   61     KNGGITYANMMSIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDEGSKSL   120

Query   214   LGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPLQSFM   273
        LGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTTISS LQSFM
Sbjct   121   LGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQQTVDGKDVYTTISSTLQSFM   180

Query   274   ETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNY   333
        ETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVWRDILYQSNY
Sbjct   181   ETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITEDFVWRDILYQSNY   240

Query   334   EPGSTMKVMMLAAIDNNTFPGGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGFA   393
        EPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT G MMTF QGFA
Sbjct   241   EPGSAMKVMTLASSIDNNTFPSGGEYFNSSEFKIADATTRDWDVNDGLTTGGMMTFLLQGFA   300

Query   394   HSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQG   453
        HSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQG
Sbjct   301   HSSNVGMSLLEQKMGDATWLDYLKRFKFGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQG   360

Query   454   ISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSFDAASLTRT   513
Sbjct   361   ISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRN   420

Query   514   NMVLVGTDVPYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAV   573
        +M+LVGTDP+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG T+YIFS V
Sbjct   421   HMILVGTDPLYGTMYNHSTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVV   480

Query   574   SMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQ   633
        +M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMKDSLNLQTTAKALEQVSQQ
Sbjct   481   TMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKDSLNLQTTAKALEQVSQQ   540

Query   634   SPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKA   693
        SPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLILSDK
Sbjct   541   SPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLILSDKV   600

Query   694   EEVPDAMYGWTKEATAETLAKWLNIELEFQSGSGSTVQKQDVRRANTAIKDIKKITLTLGD   750
        EEVPDAMYGWTKEATAETLAKWLNIELEFQSGSGSTVQKQDVRRANTAIKDIKKITLTLGD
Sbjct   601   EEVPDAMYGWTKEATAETLAKWLNIELEFQSGSGSTVQKQDVRRANTAIKDIKKITLTLGD   657

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>gb|AA556848.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=671

Score = 1180 bits (3052), Expect = 0.0, Method: Composition-based stats.
Identities = 607/671 (90%), Positives = 638/671 (95%), Gaps = 0/671 (0%)

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Query   80    YDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVRE   139
Sbjct   1      YDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVRE   60

Query   140   QLSQPNLKQVSFGAKNGGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIG   199
        QLSQPNLKQVSFGAKNGGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIG
Sbjct   61     QLSQPNLKQVSFGAKNGGITYANMMAIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIG   120

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Query	200	LAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGK	259
Sbjct	121	LAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR+GNIVPGTE VSQ+T+DGK	180
Query	260	DVYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGIT	319
Sbjct	181	DVYTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTK+GIT	240
Query	320	EDFVWRDILYQSNYEPGSTMKVMMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWDVNEG	379
Sbjct	241	+DFVWRDILYQ NYEPGS MKVM LA++IDNNTFPGGE FNSSE KIAD T RDWDVNEG	300
Query	380	LTGGRRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPA	439
Sbjct	301	LTGG MMTFSQGFHSSNVGM LLE+KMGD TWLDYLNRFKFGVPTRFGLTDEYAGQLPA	360
Query	440	DNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIV	499
Sbjct	361	DNIV+IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI+A+YDPNDQT RKSQKEIV	420
Query	500	GNPVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNG	559
Sbjct	421	GNPVSKDAAS TRT MVLVGTDPVYGTMYNHSTGKP VTPVQONVALKSGTAQIADEKNG	480
Query	560	GVLVGLTDYIIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSL	619
Sbjct	481	GVLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLN	540
Query	620	LQTTAKALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKN	679
Sbjct	541	LQ+ AK L+QV+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTKIK +S EEGKN	600
Query	680	LAPNQVLLISDKAEVDPMYGWTKETAE TLAKWLNIELEFQGS GSTVQKQDVRNTAIK	739
Sbjct	601	LAPNQVLL+LSDK EE+PDYMGW KETAE AKWL+IELEF+GSGS VQKQDVR NTAIK	660
Query	740	DIKKITLTLGD 750	
Sbjct	661	+IKKI LTLGD 671	

>emb|CAB65446.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1179 bits (3051), Expect = 0.0, Method: Composition-based stats.
Identities = 608/666 (91%), Positives = 638/666 (95%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKNGGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFG+KNGGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW	324
Sbjct	181	ISSPLQSFMETQMDAF+EKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW	240
Query	325	RDILYQSNYEPGSTMKVMMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGG	384
Sbjct	241	RDILYQSNYEPGS MKVMMMLAAAIIDNNTFPGGEVFNSSSELKIAD TIRDW+VNEGLTGG	300
Query	385	MMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVTRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGV TRFGLTDEYAGQLPADNIVN	360
Query	445	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504
Sbjct	361	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI+A+YDPN+QT R+SQKEIVGNPVS	420
Query	505	KDAASLRTTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGYLVG	564
Sbjct	421	KDAA TRT+MVLVGTDP YGTMYNHSTGK TV VPGONVALKSGTA+IADEKNGGYLVG	480
Query	565	LTDYIIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA	624
Sbjct	481	T+ IFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ A	540
Query	625	KALEQVSQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQ	684
		K L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTKIK +S EEG NLAPNQ	

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*   Sbjct   541   KNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGTNLAPNQ   600
      Query   685   QVLILSDKAEVDPDYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKI   744
                        QVL+LSDK EE+PDYMGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI
*   Sbjct   601   QVLLLSDKVEEIPDYGWKKETAETFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNIKKI   660
      Query   745   TLTLGD   750
                        LTLGD
      Sbjct   661   KLTLGD   666

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>gb|AAN32859.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

Score = 1176 bits (3043), Expect = 0.0, Method: Composition-based stats.
Identities = 606/661 (91%), Positives = 634/661 (95%), Gaps = 0/661 (0%)

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Query   90   DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV   149
      Sbjct   1   DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV   60
Query   150   SFGAKGNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG   209
      Sbjct   61   SFG+KGNGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG   120
Query   210   SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTISSPL   269
      Sbjct   121  SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVTYTTISSPL   180
Query   270   QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY   329
      Sbjct   181  QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY   240
Query   330   QSNYEPGSTMKVMMMLAAAI DNNTFPGGEVFNSSSELKIADAT'IRDWDVNEGLTGGRMMTFS   389
      Sbjct   241  QSNYEPGSAMKVMMMLAAAI DNNTFPGGEVFNSSSELKIADVTIRDWDVNEGLTGGRMMTFS   300
Query   390   QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS   449
      Sbjct   301  QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS   360
Query   450   FGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAAAS   509
      Sbjct   361  FGQGISVTQTQMIRAFTAIANDGVMLEPKFITALYDPNNQTVRRSQKEIVGNPVSKDAAAG   420
Query   510   LTRTNMVLVGTDPVYGYTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGYLVGLTDYI   569
      Sbjct   421  QTRTHMVLVGTDPRYGYTMYNHSTGKATVNVPGQONVALKSGTAEIADEKNGGYLVGSTNNI   480
Query   570   FSAVMSSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ   629
      Sbjct   481  FSVVAMNPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ AK L++   540
Query   630   VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLIL   689
      Sbjct   541  VTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGTNLAPNQVLLLL   600
Query   690   SDKAEVDPDYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLG   749
      Sbjct   601  SDKVEEIPDYGWKKETAETFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNIKKIKLTLG   660
Query   750   D   750
      Sbjct   661   D   661

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>gb|AA556854.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=666

Score = 1174 bits (3038), Expect = 0.0, Method: Composition-based stats.
Identities = 607/665 (91%), Positives = 637/665 (95%), Gaps = 0/665 (0%)

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Query   86   PIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPN   145
      Sbjct   2   PIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPN   61
Query   146   LKQVSFGAKGNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLAQLHE   205
      Sbjct   62   LKQVSFGAKGNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLAQLHE   121
Query   206   NEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTYTTI   265
      Sbjct   122  NEDGSKSLLGT G+ESSLN+ILAGTDGIITYEKDR+GNIVPGTE VSQ+T+DGKDVTYTT+   181
Query   266   SSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWR   325
      Sbjct   266  SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTK+GIT+DFVWR

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Sbjct	182	SSPLQSFMETQMDAFLEKVKGYMTATLVSAKTGEILATTQRPTFNADTKDGITKDFVWR	241
Query	326	DILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRM	385
Sbjct	242	DILYQ NYEPGS MKVM LA++IDNNTFPGGE FNSSE KIAD T RDWDVNEGLTGG M	301
Query	386	MTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNI	445
Sbjct	302	MTFSQGFAHSSNVGM LLE+KMGD TWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIV+I	361
Query	446	AQSSFQGGISVTTQTMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSK	505
Sbjct	362	AQSSFQGGISVTTQTMIRAFATAIANDGVMLEPKFI+A+YDPNDQT RKSQKEIVGNPVSK	421
Query	506	DAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQGQNALVKSQTAAQIADEKNGGYLVGL	565
Sbjct	422	DAASQTRTQMVLVGTDPVYGTMYNHSTGKPIVTVPGQNALVKSQTAAQIADEKNGGYLVGP	481
Query	566	TDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAK	625
Sbjct	482	TNYIFSVVAMNPAENPDFILYVTVQQPEH+SGIQLGEFANPILERASAMK+SLNLQ+ AK	541
Query	626	ALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQ	685
Sbjct	542	L+QV+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTKIK +S EEGKNL+PNQQ	601
Query	686	VLILSDKAEVDPMYGWTKETATLAKWLNIELEFQSGSGSTVQKQDVRRANTAIKDIKKIT	745
Sbjct	602	VLILSDKAEVDPMYGWTKETATLAKWLNIELEF+GSGSGSTVQKQDVRRANTAIKDIKKIT	661
Query	746	LTLGD 750	
Sbjct	662	LTLGD 666	

>gb|AAN32860.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

Score = 1174 bits (3038), Expect = 0.0, Method: Composition-based stats.
Identities = 609/661 (92%), Positives = 635/661 (96%), Gaps = 0/661 (0%)

Query	90	DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV	149
Sbjct	1	DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV	60
Query	150	SFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG	209
Sbjct	61	SFG+KNGGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG	120
Query	210	SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPL	269
Sbjct	121	SKSLLGTSGMESSLNSILAG DGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTTISS L	180
Query	270	QSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY	329
Sbjct	181	QSFMETQM+AFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEG+T+DFVWRDILY	240
Query	330	QSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFS	389
Sbjct	241	QSNYEPGSTMKVM LAAAIIDNNTFPGGEVFNSSSELK+ADATIRDWDVNEGLTGG MMTFS	300
Query	390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct	301	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGI PTRFGLTDEYAGQLPADNIVNIAQSS	360
Query	450	FGQGISVTTQTMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAAS	509
Sbjct	361	FGQGISVTTQTMIRAFATAIANDGVMLEPKFI+A+YDPN+Q+ RKSQKEIVGNPVSKDAAS	420
Query	510	LTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQGQNALVKSQTAAQIADEKNGGYLVGLTDYI	569
Sbjct	421	TRT+MVLVGTDP YGTMYNHSTGK TV VPGQNALVKSQTAAQIADEKNGGYLVG T+ I	480
Query	570	FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ	629
Sbjct	481	FS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERA AMKDSLNLQ+TAK L+Q	540
Query	630	VSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLIL	689
Sbjct	541	V+ QS Y MPS+KDISPGDLAE LRRN+VQPIVVGTGTKIK SS EEG NLAPNQVLL+L	600
Query	690	SDKAEVDPMYGWTKETATLAKWLNIELEFQSGSGSTVQKQDVRRANTAIKDIKKITLTLG	749
Sbjct	601	SDKAEVDPMYGWT KATAEAFSKWLNIELVFEGSGSGSTVQKQDVRRANTAIKDIKKITLTLG	660
Query	750	D 750	

Sbjct 661 D 661

>gb|AA556839.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=670

Score = 1170 bits (3027), Expect = 0.0, Method: Composition-based stats.
Identities = 603/670 (90%), Positives = 636/670 (94%), Gaps = 0/670 (0%)

Query	81	DRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ	140
Sbjct	1	DRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ	60
Query	141	LSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGL	200
Sbjct	61	LSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGL	120
Query	201	AQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKD	260
Sbjct	121	AQLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKD	180
Query	261	VYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITE	320
Sbjct	181	VYTTISSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITE	240
Query	321	DFVWRDILYQSNYEPGSTMKVMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGL	380
Sbjct	241	DFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFNSSEFKIADATTRDWDVNDGL	300
Query	381	TGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTFRGLTDEYAGQLPAD	440
Sbjct	301	TGGRMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLNRFKFGVPTFRGLTDEYAGQLPAD	360
Query	441	NIVNIAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVG	500
Sbjct	361	NIVNIAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVG	420
Query	501	NPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGG	560
Sbjct	421	NPVSKAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGG	480
Query	561	YLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNL	620
Sbjct	481	YLVGSTNYIFSVVMTMNAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNL	540
Query	621	QTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAAEEGKNL	680
Sbjct	541	QTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAAEEGKNL	600
Query	681	APNQOVLILSDKAAEVPDYGWTKETAETLAKWLNIELEFGSGSTVQKQDVRRANTAIKD	740
Sbjct	601	APNQOVLILSDKAAEVPDYGWTKETAETLAKWLNIELEFGSGSTVQKQDVRRANTAIKD	660
Query	741	IKKITLTLGD 750	
Sbjct	661	IKKITLTLGD 670	

>emb|CAB65445.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1170 bits (3026), Expect = 0.0, Method: Composition-based stats.
Identities = 599/665 (90%), Positives = 636/665 (95%), Gaps = 0/665 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT	264
Sbjct	121	ENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEFVW	324
Sbjct	181	ISSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKDGITKDFVW	240
Query	325	RDILYQSNYEPGSTMKVMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGR	384
Sbjct	241	RDILYQSNYEPGSAMKVMTLAASIDNNTFPGGEVFNSSSELKIADATIRDWDVNDGLTTGG	300
Query	385	MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTFRGLTDEYAGQLPADNIVN	444

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Sbjct 301 MMTFSQGFAHSSNVGM+LLEQKMGD TWLDYLNRFKFGVPTRFGLTDEY+GQLPADNIVN 360
MMTFSQGFAHSSNVGMSLLEQKMGD TTWLDYLNRFKFGVPTRFGLTDEYSGQLPADNIVN

Query 445 IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS 504
IA S+FGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVG PVS
Sbjct 361 IAMSAFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGKPV 420
IAMS+FGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYD TNNQSVRKSQKEIVGKPV

Query 505 KDAASLRTNMTMLVLTGDPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVG 564
+DAASLRTNMTMLVLTGDP+YGTMYNH TGKP +TVPGQNVALKSGTA+IADEKNGGYLVG
Sbjct 421 EDAASLRTNMTMLVLTGDPYGTMYNHYTGKPIITVPQNVALKSGTAETIADEKNGGYLVG 480
EDAASLRTNMTMLVLTGDPYGTMYNHYTGKPIITVPQNVALKSGTAETIADEKNGGYLVG

Query 565 LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA 624
T+YIF V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ A
Sbjct 481 STNYIFPVVMTMNPENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNLQSPA 540
STNYIFPVVMTMNPENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNLQSPA

Query 625 KALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTTIKNSSAEEGKNLAPNQ 684
K L+QV+ +S Y MPS+KDISPGDLAE LRRN+VQPIVVGTGTTIK SS EEG NLAPNQ
Sbjct 541 KNLDQVTTTESSYAMPSIKDISPGDLAEALRRNIVQPIVVGTGTTIKESSVEEGTNLAPNQ 600
KNLDQVTTTESSYAMPSIKDISPGDLAEALRRNIVQPIVVGTGTTIKESSVEEGTNLAPNQ

Query 685 QVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGTVQKQDVRRANTAIKDIKKI 744
QV++LSDK EE+PDMYGW KETAET AKWLNIELEF+GSGSGTVQKQDVRRANTAIKDIKKI
Sbjct 601 QVLLSDKVEEIPDMYGWKKETAETFAKWLNIELEFEGSGSGTVQKQDVRRANTAIKDIKKI 660
QVLLSDKVEEIPDMYGWKKETAETFAKWLNIELEFEGSGSGTVQKQDVRRANTAIKDIKKI

Query 745 TLTLG 749
TLTLG
Sbjct 661 TLTLG 665
TLTLG

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>emb|CAA67013.1| penicillin-binding protein [Streptococcus pneumoniae]
Length=666

Score = 1169 bits (3024), Expect = 0.0, Method: Composition-based stats.
Identities = 602/666 (90%), Positives = 633/666 (95%), Gaps = 0/666 (0%)

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Query 85 VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP 144
VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYL MEESYVREQLSQP
Sbjct 1 VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLAMEESYVREQLSQP 60
VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLAMEESYVREQLSQP

Query 145 NLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH 204
NLKQVSFGAKGNGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH
Sbjct 61 NLKQVSFGAKGNGITYANMMAIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH 120
NLKQVSFGAKGNGITYANMMAIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH

Query 205 ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR LGNIVPGTEQVSQRTMDGKDVYTT 264
ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR+GNIIVPGTE VSQ+T+DGKDVYTT
Sbjct 121 ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRVGNIVPGTELVVSQQTVDGKDVYTT 180
ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRVGNIVPGTELVVSQQTVDGKDVYTT

Query 265 ISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITDFVW 324
+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTK+GIT+DFVW
Sbjct 181 LSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKDGITKDFVW 240
LSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKDGITKDFVW

Query 325 RDILYQSNYEPGSTMKVMMMLAAAIDNNTFPGGEVFNSSSELKIADATIRDWVNEGLTGGR 384
RDILYQ NYEPGS MKVMMMLA++IDNNTFPGGE FNSSE KIAD T RDWVNEGLTGGR
Sbjct 241 RDILYQGNYEPGSAMKVMMMLASSIDNNTFPGGEYFNSSSESKIADVTTTRDWVNEGLTGGG 300
RDILYQGNYEPGSAMKVMMMLASSIDNNTFPGGEYFNSSSESKIADVTTTRDWVNEGLTGGG

Query 385 MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN 444
MMTFSQGFAHSSNVGM LLE+KMGD TWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIV+
Sbjct 301 MMTFSQGFAHSSNVGMILLEEKMGD TTWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVS 360
MMTFSQGFAHSSNVGMILLEEKMGD TTWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVS

Query 445 IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS 504
IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI+A+YDPNDQT RKSQKEIVGNPVS
Sbjct 361 IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFITALYDPNDQTVRKSQKEIVGNPVS 420
IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFITALYDPNDQTVRKSQKEIVGNPVS

Query 505 KDAASLRTNMTMLVLTGDPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGGYLVG 564
KDAAS TRT MVLVLTGDPVYGTMYNHSTGKP VTVPQNVALKSGTAQIADEKNGGYLVG
Sbjct 421 KDAASQTRTQMVLVLTGDPVYGTMYNHSTGKPIVTVPGQNVALKSGTAQIADEKNGGYLVG 480
KDAASQTRTQMVLVLTGDPVYGTMYNHSTGKPIVTVPGQNVALKSGTAQIADEKNGGYLVG

Query 565 LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA 624
T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ A
Sbjct 481 PTNYIFSVMNPENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNLQSPA 540
PTNYIFSVMNPENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNLQSPA

Query 625 KALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTTIKNSSAEEGKNLAPNQ 684
K L+QV+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTTIK +S EEGKNLAPNQ
Sbjct 541 KNLDQVTTTESSYAMPSIKDISPGELAE LRRNIVQPIVVGTGTTIKETSVEEGKNLAPNQ 600
KNLDQVTTTESSYAMPSIKDISPGELAE LRRNIVQPIVVGTGTTIKETSVEEGKNLAPNQ

Query 685 QVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGTVQKQDVRRANTAIKDIKKI 744
QVL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI
Sbjct 601 QVLLSDKVEEIPDMYGWKKETAETFAKWLDIELEFEGSGSIVQKQDVRTNTAIKNIKKI 660
QVLLSDKVEEIPDMYGWKKETAETFAKWLDIELEFEGSGSIVQKQDVRTNTAIKNIKKI

Query 745 TLTLGD 750
LTLGD
Sbjct 661 KLTLGD 666
KLTLGD

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>gb|AA556838.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=670

Score = 1165 bits (3014), Expect = 0.0, Method: Composition-based stats.
Identities = 601/670 (89%), Positives = 635/670 (94%), Gaps = 0/670 (0%)

Query	81	DRNGVPVIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ	140
Sbjct	1	DRNGVPVIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ	60
Query	141	LSQPNLKQVSFGAKNGGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGL	200
Sbjct	61	LSQPNLKQVSFGAKNGGITYANMMSIKKELEAEVKGIDFTTSPNRSYPNGQFASSFIGL	120
Query	201	AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKD	260
Sbjct	121	AQLHENEDGSKSLLGTSGMESSLNSILAGDGIITYEKDRLGNIVPGTEQVSQ+T+DGKD	180
Query	261	VYTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITE	320
Sbjct	181	VYTTISSLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFNADTKEGITE	240
Query	321	DFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFNSELKIADATIRDWDVNEGL	380
Sbjct	241	DFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPGGEVFNSEFKIADATIRDWDVNDGL	300
Query	381	TGGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTFRGLTDEYAGQLPAD	440
Sbjct	301	TGGRMMTFLQGFHSSNVGMSLLEQKMGDATWLDYLNRFKFGVPTFRGLTDEYAGQLPAD	360
Query	441	NIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVG	500
Sbjct	361	NIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVG	420
Query	501	NPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGG	560
Sbjct	421	NPVSKAAASTTRNHMILVGTDPVYGTMYNHYTGKPIITVPGQNVAVKSGTAQIADEKNGG	480
Query	561	YLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNL	620
Sbjct	481	YLVGSTNYIFSVVTMNPENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNL	540
Query	621	QTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGKTIKNSSAEEGKNL	680
Sbjct	541	QSPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNLVQPIVVGTGKTIKETSVEEGTNL	600
Query	681	APNQQVLILSDKAEVPMYGTWKETAETLAKWLNIELEFGSGSTVQKQDVRANTAIKD	740
Sbjct	601	APNQQVLLLSDKVEEIPMYGWWKETAETFAKWLIDIELEFEGSGSVVQKQDVRANTAIKD	660
Query	741	IKKITLTLGD 750	
Sbjct	661	IKKITLTLGD 670	

>emb|CAB65442.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1165 bits (3014), Expect = 0.0, Method: Composition-based stats.
Identities = 597/666 (89%), Positives = 630/666 (94%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKNGGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFG+KNGGITYANMMSIKKELEAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFW	324
Sbjct	181	ISSTLQSFMETQMNAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITKDFW	240
Query	325	RDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFNSELKIADATIRDWDVNEGLTGGR	384
Sbjct	241	RDILYQSNYEPGSTMKVM LA++IDNNTFP GE FNSSE KIAD TIRDWDVN GLT GR	300
Query	385	MMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTFRGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTFLQGFALSSNVGMSLLEQKMGDATWLDYLNRFKFGVPTFRGLTDEYAGQLPADNIVN	360
Query	445	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504
Sbjct	361	IAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFITALYDPNDQTVRRSQKEIVGNPVS	420

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Query   505   KDAASLRTNMTVLVGTDPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG   564
          KDAASLRT+MVLVGTDP YGTMYNH TGKP +TVPGQNVA+KSGTA+IADEKNGGYLVG
Sbjct   421   KDAASLRTHTMVLVGTDPYGTMYNHGTGKPIITVPGQNVAVKSGTAEIADEKNGGYLVG   480

Query   565   LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA   624
          T+YIFS VSM+PAENPDFILYVT+QQPEHYS + LGEFANPILERASAMK+SLNLQ+ A
Sbjct   481   ATNYIFSVMNPAENPDFILYVTIQQPEHYSVVHLGEFANPILERASAMKESLNLQSPA   540

Query   625   KALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTTGKTIKNSSAEEGKNLAPNQ   684
          K LEQV+ +S Y MPS+KDISPGDLAE LRRN+VQPIV+GTGKTIK SS EEGKNL PNQ
Sbjct   541   KNLEQVTAESSYAMPSIKDISPGDLAEALRRNIVQPIVIGTGTIKIKESSVEEGKNLVPNQ   600

Query   685   QVLILSDKAAEEVPDYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRRANTAIKDIKKI   744
          QVL+LSDK EE+PDYMGW KETAE AKWL+IELEF+GSGS VQ+QDVRRANT IK+IK I
Sbjct   601   QVLLLSDKVEEIPDYGWKKETAEAFKWLKDIELEFEGSGSIVQKQDVRRANTTIKNIKNI   660

Query   745   TLTLGD   750
          LTLGD
Sbjct   661   KLTLGD   666

```

>emb|CAB65443.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1162 bits (3007), Expect = 0.0, Method: Composition-based stats.
Identities = 601/666 (90%), Positives = 634/666 (95%), Gaps = 0/666 (0%)

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Query   85   VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP   144
          VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP
Sbjct   1     VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP   60

Query   145  NLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH   204
          NLKQVSFGAKGNGITYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH
Sbjct   61   NLKQVSFGAKGNGITYANMMSIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH   120

Query   205  ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT   264
          ENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTT
Sbjct   121  ENEDGSKSLLGTSGMESSLNSILAGKDGIIITYEKDRLGNIVPGTEQVSQQTVDGKDVYTT   180

Query   265  ISSPLQSFQMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEFVW   324
          ISS LQSFQMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEG+T+DFVW
Sbjct   181  ISSTLQSFQMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGLTKDFVW   240

Query   325  RDILYQSNYEPGSTMKVMMLAAIDNNTFPGGEVFNSELKIADATIRDWDVNEGLTGGRR   384
          RDILYQSNYEPGSTMKVM LA++ID+NTFP GE FNSSELKIADATIRDWDVN+GLT G
Sbjct   241  RDILYQSNYEPGSTMKVMTLASSIDSNTFPGGEVFNSELKIADATIRDWDVNDGLTTGG   300

Query   385  MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN   444
          MMTF QGFA+SSNVGM+LLEQKMGDATWLDYLNRFKFGVPTRFGLTDEY+GQLPADNIVN
Sbjct   301  MMTFLQGFAYSNVGMSSLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYSGQLPADNIVN   360

Query   445  IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS   504
          IA S+FGQGISVTQTQM+RAFTAIANDGVMLEPKFISA+YDPNDQT RKSQKEIVGNPVS
Sbjct   361  IAMSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISALYDPNDQTVRKSQKEIVGNPVS   420

Query   505  KDAASLRTNMTVLVGTDPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG   564
          KDAAS TRT+MVLVGTDP YGTMYNHSTGK TV VPGQNVALKSGTA+IADEKNGGYLVG
Sbjct   421  KDAASQTRTHMVLVGTDPYGTMYNHSTGKATVNVPGQNVALKSGTAEIADEKNGGYLVG   480

Query   565  LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA   624
          T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ A
Sbjct   481  STNYIFSVMNPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKESLNLQSPA   540

Query   625  KALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTTGKTIKNSSAEEGKNLAPNQ   684
          K L+QV+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTTGKTIK +S EEGKNLAPNQ
Sbjct   541  KNLDQVTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTTGKTIKETSVEEGKNLAPNQ   600

Query   685  QVLILSDKAAEEVPDYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDVRRANTAIKDIKKI   744
          QVL+LSDK EE+PDYMGW KETAE AKWL+IELEF+GSGS VQKQDVRR NTAIK+IKKI
Sbjct   601  QVLLLSDKVEEIPDYGWKKETAEAFKWLKDIELEFEGSGSIVQKQDVRRNTAIKNIKKI   660

Query   745  TLTLGD   750
          LTLGD
Sbjct   661  KLTLGD   666

```

>gb|AA56842.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=669

Score = 1160 bits (3000), Expect = 0.0, Method: Composition-based stats.
Identities = 597/669 (89%), Positives = 633/669 (94%), Gaps = 0/669 (0%)

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Query   82   RNVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL   141
          RNVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL
Sbjct   1     RNVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL   60

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Query   142   SQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLA 201
Sbjct   61     SQPNLKQVSFGAKGNGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLA 120
SQPNLKQVSFGAKGNGITYANMMAIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIGLA

Query   202   QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV 261
Sbjct   121   QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDV 180
QLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDV

Query   262   YTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPFTDADTKEGITED 321
Sbjct   181   YTTISSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPFT+ADTKEGITED 240
YTTISSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPFTNADTKEGITED

Query   322   FVWRDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLT 381
Sbjct   241   FVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT 300
FVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFNSSEFKIADATTRDWDVNDGLT

Query   382   GGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN 441
Sbjct   301   TGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRKFKFGVPTRFGLTDEYAGQLPADN 360
G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADN

Query   442   IVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQQEIVGN 501
Sbjct   361   IV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQQEIVGN 420
IVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQQEIVGN

Query   502   PVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGGY 561
Sbjct   421   PVSKEAASSTRNHMILVGTDPVYGTMYNHYTGKPIITVPQONVAVKSGTAQIADEKNGGY 480
PVSK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVPGQONVA+KSGTAQIADEKNGGY

Query   562   LVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ 621
Sbjct   481   LVGSTNYIFSVVTMNPANPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQ 540
LVGLT+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQ

Query   622   TTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLA 681
Sbjct   541   + AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTKIK +S EEG NLA 600
SPAKNLDKVTTESYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGTNLA

Query   682   PNQQVLLISDKAEVDPMYGWTKETATLAKWLNIELEFQSGSGSTVQKQDVRANTAIDKI 741
Sbjct   601   PNQQVLL+LSDK EE+PDYMGW KETAT AKWL+IELEF+GSGS VQKQDVR NTAIK+I 660
PNQQVLLLSDKVEEIPDYGWKKETATFAKWLIDIELEFEGSGSVVQKQDVRTNTAIKNI

Query   742   KKITLTLGD 750
Sbjct   661   KKI LTLGD 669
KKIKLTLGD

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>gb|AA56852.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=670

Score = 1158 bits (2996), Expect = 0.0, Method: Composition-based stats.
Identities = 596/670 (88%), Positives = 632/670 (94%), Gaps = 0/670 (0%)

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Query   81     DRNGVPPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ 140
Sbjct   1      DRNGVPPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ 60
DRNGVPPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQ

Query   141   LSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGL 200
Sbjct   61     LSQPNLKQVSFGAKGNGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGL 120
LSQPNLKQVSFGAKGNGITYANMMTIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIGL

Query   201   AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKD 260
Sbjct   121   AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTE VSQ+T+DGKD 180
AQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTELVSQQTVDGKD

Query   261   VYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPFTDADTKEGITE 320
Sbjct   181   VYTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPFT+ADTKEGITE 240
VYTTLSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPFTNADTKEGITE

Query   321   DFVWRDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGL 380
Sbjct   241   DFVWRDILYQSNYEPGS KVMMLA++IDNNTFP GE FNSSE KIADAT RDWDVNEGL 300
DFVWRDILYQSNYEPGSFAKVMMLASSIDNNTFPSGEYFNSSEFKIADATTRDWDVNEGL

Query   381   TGGMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPAD 440
Sbjct   301   TGGMMTFSQGFAHSSNVGTSLLLEQKMGDATWLDYLRKFKFGVPTRFGLTDEYAGQLPAD 360
T G MMTFSQGFAHSSNVG +LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPAD

Query   441   NIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQQEIVG 500
Sbjct   361   NIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQQEIVG 420
NIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQQEIVG

Query   501   NPVSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQONVALKSGTAQIADEKNGG 560
Sbjct   421   NPVSK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVPGQONVA+KSG AQIADEKNGG 480
NPVSKEAASSTRNHMILVGTDPVYGTMYNHYTGKPIITVPQONVAVKSGAAQIADEKNGG

Query   561   YLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNL 620
Sbjct   481   YLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNL 540
YLVGSTNYIFSVVTMNPANPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNL

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Query   621  QTTAKALEQVSQQSPYPMPVSKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNL 680
      Q+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTKIK +S EEG NL
Sbjct   541  QSPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGTNL 600

Query   681  APNQQVLILSDKAAEEVPDYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDV RANTAIKD 740
      APNQQVL+LSDK EE+PDYMGW KETAET AKWL+IELEF+GSGS VQKQDV R NTAIK+
Sbjct   601  APNQQVLLLSDKVVEEIPDYGWKKETAETFAKWLDIELEFEGSGSVVQKQDV RNTAIKN 660

Query   741  IKKITLTLGD 750
      IKKI LTLGD
Sbjct   661  IKKIKLTLGD 670

```

>emb|CAB65441.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1157 bits (2992), Expect = 0.0, Method: Composition-based stats.
Identities = 597/666 (89%), Positives = 631/666 (94%), Gaps = 0/666 (0%)

```

Query   85  VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP 144
      VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP
Sbjct   1  VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP 60

Query   145  NLKQVSFGAKGNGITYANMMSIKKELEAAEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLH 204
      NLKQVSFGAKGNGITYANMMSIKKELE AEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLH
Sbjct   61  NLKQVSFGAKGNGITYANMMSIKKELETAEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLH 120

Query   205  ENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT 264
      ENEDGSKSLGTSGMESSLNSILAG DGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTT
Sbjct   121  ENEDGSKSLGTSGMESSLNSILAGKDGIIITYEKDRLGNIVPGTEQVSQQTVDGKDVYTT 180

Query   265  ISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW 324
      ISS LQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVW
Sbjct   181  ISSTLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFNADTKEGITEDFVW 240

Query   325  RDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGR 384
      RDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT G
Sbjct   241  RDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFNSSSEFKIADATTRDWDVNDGLTTGG 300

Query   385  MMTFSQGFHSSNVGMLTLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN 444
      MMTF QGFHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+
Sbjct   301  MMTFLQGFHSSNVGMSLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVS 360

Query   445  IAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS 504
      IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVS
Sbjct   361  IAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVS 420

Query   505  KDAASLRTNMVLVGTDVPYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG 564
      K+AAS TR +M+LVGTDV+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG
Sbjct   421  KEAASLRTNMILVGTDPLYGTMYNHYTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVG 480

Query   565  LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA 624
      T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ A
Sbjct   481  STNYIFSVMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQSPA 540

Query   625  KALEQVSQQSPYPMPVSKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQ 684
      K L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTKIK +S EEG NLAPNQ
Sbjct   541  KNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGTNLAPNQ 600

Query   685  QVLILSDKAAEEVPDYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDV RANTAIKDIKKI 744
      QVL+LSDK EE+PDYMGW KETAET AKWL+IELEF+GSGS VQKQDV RANTAIKDIKKI
Sbjct   601  QVLLLSDKVVEEIPDYGWKKETAETFAKWLDIELEFEGSGSVVQKQDV RANTAIKDIKKI 660

Query   745  TLTLGD 750
      TLTLGD
Sbjct   661  TLTLGD 666

```

>gb|AAN32855.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

Score = 1157 bits (2992), Expect = 0.0, Method: Composition-based stats.
Identities = 598/661 (90%), Positives = 630/661 (95%), Gaps = 0/661 (0%)

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Query   90  DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV 149
      DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV
Sbjct   1  DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV 60

Query   150  SFGAKGNGITYANMMSIKKELEAAEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLH NEDG 209
      SFGAKGNGITYANMMSIKKELE AEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLH NEDG
Sbjct   61  SFGAKGNGITYANMMSIKKELETAEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLH NEDG 120

Query   210  SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPL 269
      SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTTISS L
Sbjct   121  SKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDVYTTISSTL 180

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Query	270	QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY	329
Sbjct	181	QSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEG+T+DFVWRDILY	240
Query	330	QSNYEPGSTMKVMMLAAAIIDNNTFPGGGEVFNSELKIADATIRDWDVNEGLTGGRMMTFS	389
Sbjct	241	QSNYEPGSTMKVM LA++IDNNTFP GE FNSSELKIADATIRDWDVN+GLT G MMTF	300
Query	390	QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS	449
Sbjct	301	QGFAHSSNVGMSLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYSGQLPADNIVNIAMSA	360
Query	450	FGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSCKDAAS	509
Sbjct	361	FGQGISVTQTQM+RAFAATAIANDGVMLEPKFISAIYDPNDQT RKSQKEIVGNPVSCKDAAS	420
Query	510	LTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYI	569
Sbjct	421	QTRTHMVLVGTDPRYGTMYNHSTGKATVNVPGQNVALKSGTAEIADEKNGGYLVGSTNYI	480
Query	570	FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ	629
Sbjct	481	FS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMK+SLNLQ+ AK L+Q	540
Query	630	VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTTGKTIKNSAEEGKNLAPNQVLLIL	689
Sbjct	541	V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTTGKTIK +S EEGKNLAPNQVLL+L	600
Query	690	SDKAEVVPDMPYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRNTAIKDIKKITLTG	749
Sbjct	601	SDK EE+PDMPYGTWKETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI LTG	660
Query	750	D 750	
Sbjct	661	D 661	

>gb|AA56849.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=669

Score = 1155 bits (2987), Expect = 0.0, Method: Composition-based stats.
Identities = 594/669 (88%), Positives = 632/669 (94%), Gaps = 0/669 (0%)

Query	82	RNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL	141
Sbjct	1	RNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL	60
Query	142	SQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLA	201
Sbjct	61	SQPNLKQVSFG+KNGNGITYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLA	120
Query	202	QLHENEDGSKSLLGTSGMESSLSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV	261
Sbjct	121	QLHENEDGSKSLLGTSGMESSLSILAGTDGIITYEKDR+GNIVPGTE VSQ+T+DGKDV	180
Query	262	YTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITED	321
Sbjct	181	YTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITED	240
Query	322	FVWRDILYQSNYEPGSTMKVMMLAAAIIDNNTFPGGGEVFNSELKIADATIRDWDVNEGLT	381
Sbjct	241	FVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT	300
Query	382	GGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN	441
Sbjct	301	G MMTF QGFAHSSNVGMSLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN	360
Query	442	IVNIAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGN	501
Sbjct	361	IV+IAQSSFGQGISVTQTQM+RAFAATAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGN	420
Query	502	PVSCKDAASLRTTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGY	561
Sbjct	421	PVSCKAAS TR +M+LVGTDVP+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGY	480
Query	562	LVGLTDYIIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ	621
Sbjct	481	LVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ	540
Query	622	TTAKALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTTGKTIKNSAEEGKNLA	681
Sbjct	541	+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTTGKTIK +S EEG NLA	600
Query	682	PNQQVLLILSDKAEVVPDMPYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRNTAIKDI	741
		PNQQVL+LSDK EE+PDMPYGTWKETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+I	

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* Sbjct 601 PNQQVLLLSDKVEEIPDMYGWKKETAETFAKWLDDIELEFEGSGSVVQKQDVRTNTAIKNI 660
Query 742 KKITLTLGD 750
      KKI LTLGD
- Sbjct 661 KKIKLTLGD 669

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>gb|AA556851.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=668

Score = 1152 bits (2980), Expect = 0.0, Method: Composition-based stats.
Identities = 593/668 (88%), Positives = 631/668 (94%), Gaps = 0/668 (0%)

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Query 83  NGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLS 142
Sbjct 1   NGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLS 60

Query 143 QPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKIGIDFTTSPNRSYPNGQFASSFIGLAQ 202
Sbjct 61  QPNLKQVSFG+KNGGITYANMMSIKKELE AEVKIGIDFTTSPNRSYPNGQFASSFIGLAQ 120
      QPNLKQVSFGSKGNGITYANMMSIKKELETAEVKIGIDFTTSPNRSYPNGQFASSFIGLAQ

Query 203 LHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDR LGNIVPGTEQVSQRTMDGKDVY 262
Sbjct 121 LHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDR+GNIVPGTE VSQ+T+DGKDVY 180
      LHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRVGNIVPGTELVSQQTVDGKDVY

Query 263 TTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDF 322
Sbjct 181 TT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDF 240
      TTLSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITEDF

Query 323 VWRDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTG 382
Sbjct 241 VWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFNSSEFKIADATTRDWDVNDGLTT 300
      VWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFNSSEFKIADATTRDWDVNDGLTT

Query 383 GRMMTF SQGFAHSSNVGMTLLLEQKMGDWTWLDYLNRFKFGVPTRFGLTDEYAGQLPADNI 442
Sbjct 301 G MMTF QGFAHSSNVGM+LLEQKMGDWTWLDYL RKFVGVPTRFGLTDEYAGQLPADNI 360
      GGMMTFLQGFAHSSNVGMSLLEQKMGDWTWLDYLRKFVGVPTRFGLTDEYAGQLPADNI

Query 443 VNIAQSSFGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNP 502
Sbjct 361 V+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNP 420
      VSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNP

Query 503 VSKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQNVALKSGTAQIADEKNGGYL 562
Sbjct 421 VSK+AAS TR +M+LVGTDP+YGTMYNH TGKP +TVPQNVA+KSGTAQIADEKNGGYL 480
      VSKEAASLRTNMILVGTDPVYGTMYNHSTGKPIITVPQNVAVKSGTAQIADEKNGGYL

Query 563 VGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQT 622
Sbjct 481 VG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ 540
      VGSTNYIFSVMTPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQS

Query 623 TAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTGIKNSSAEEGKNLAP 682
Sbjct 541 AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTGIK +S EEG NLAP 600
      PAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTGIKETSVEEGTNLAP

Query 683 NQQVLILSDKAAEVPDMYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDV RANTAIKDIK 742
Sbjct 601 NQQVL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IK 660
      NQQVLLLSDKVEEIPDMYGWKKETAETFAKWLDDIELEFEGSGSVVQKQDVRTNTAIKNIK

Query 743 KITLTLGD 750
Sbjct 661 KIKLTLGD 668

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>gb|AA556841.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=674

Score = 1150 bits (2974), Expect = 0.0, Method: Composition-based stats.
Identities = 592/674 (87%), Positives = 634/674 (94%), Gaps = 0/674 (0%)

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Query 77  GTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESY 136
Sbjct 1   GTIYDRNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFNKVAEVFHKYLDME+E+Y 60
      GTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFNKVAEVFHKYLDMEDEAY

Query 137 VREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKIGIDFTTSPNRSYPNGQFASS 196
Sbjct 61  V+EQLSQPNL QVSFGAKGNGITYANMM+IKK+L+ A ++GIDFTTSPNRSYPNGQFASS 120
      VKEQLSQPNLTQVSFGAKGNGITYANMMAIKKDLKDASIEGIDFTTSPNRSYPNGQFASS

Query 197 FIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDR LGNIVPGTEQVSQRTM 256
Sbjct 121 FIGLAQLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR LGNIVPGTEQVSQ+T+ 180
      FIGLAQLHENEDGSKSLLGTSGMESSLNSILAGDKDGIITYEKDR LGNIVPGTEQVSQQT V

Query 257 DGKDVYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKE 316
Sbjct 181 DGKDVYTTISS LQSFMETQM+AF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKE 240
      DGKDVYTTISS TLQSFMETQMNAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKE

Query 317 GITEDFVWRDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDV 376
      GITEDFVWRDILYQSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDV

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Sbjct	241	GITEDFVWRDILYQSNEYPGSAMKVMTLASSIDNNTFPSGEYFNSSEFKIADATTRDWDV	300
Query	377	NEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQ N+GLT G MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQ	436
Sbjct	301	NDGLTTGGMFTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRKFKFGVPTRFGLTDEYAGQ	360
Query	437	LPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSOK LPADNIV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSOK	496
Sbjct	361	LPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSOK	420
Query	497	EIVGNPVSCKDAASLRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADE EIVGNPVSCK+AAS TR +M+LVGTDV+YGTMYNH TGKP +TVPGQNV+A+KSGTAQIADE	556
Sbjct	421	EIVGNPVSKEAASLRTNMILVGTDPLYGTMYNHSTGKPIITVPGQNVAVKSGTAQIADE	480
Query	557	KNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKD KNGGYLVG T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+	616
Sbjct	481	KNGGYLVGSTNYIFSVVTMNPENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKE	540
Query	617	SLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGKTIKNSSAEE SLNLQ+ AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGKTIK +S EE	676
Sbjct	541	SLNLQSPAKNLDDKVTTESSYAMPSIKDISPGELAEALRRNLVQPIVVGTGKTIKETSVEE	600
Query	677	GKNLAPNQVVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANT G NLAPNQVVLILSDKAEVPMYGTWKETAETLAKWLNIELEF+GSGS VQKQDVR NT	736
Sbjct	601	GTNLAPNQVVLILSDKAEVPMYGTWKETAETLAKWLNIELEFEGSGSVVQKQDVRTNT	660
Query	737	AIKDIKKITLTLGD 750 AIK+IKKI LTLGD	
Sbjct	661	AIKNIKKIKLTLGD 674	

>emb|CAA88920.1| penicillin-binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1149 bits (2973), Expect = 0.0, Method: Composition-based stats.
Identities = 592/666 (88%), Positives = 628/666 (94%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLAQLH NLKQVSFGAKGNGITYANMM+IKKELE AEVKIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNGITYANMMTIKKELETAEVKIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTE VSQ+T+DGKDVYTT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTELVSQQTVDGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW +SSPLQSFMETQMDAF EKVKGKGYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVW	324
Sbjct	181	LSSPLQSFMETQMDAFLEKVKGKGYMTATLVSAKTGEILATTQRPTFNADTKEGITEDFVW	240
Query	325	RDILYQSNEYPGSTMKVMMLAAAIDNNTFPGGGEVFNSELKIADATIRDWDVNEGLTGGR RDILYQSNEYPGS KVMMLA++IDNNTFP GE FNSSE KIADAT RDWDVNEGLT G	384
Sbjct	241	RDILYQSNEYPGSAFKVMMLASSIDNNTFPSGEYFNSSEFKIADATTRDWDVNEGLTTGG	300
Query	385	MMTFSQGFAGHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN MMTFSQGFAGHSSNVG +LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+	444
Sbjct	301	MMTFSQGFAGHSSNVGTSLLLEQKMGDATWLDYLRKFKFGVPTRFGLTDEYAGQLPADNIVS	360
Query	445	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSOKKEIVGNPVS IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSOKKEIVGNPVS	504
Sbjct	361	IAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSOKKEIVGNPVS	420
Query	505	KDAASLRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG K+AAS TR +M+LVGTDV+YGTMYNH TGKP +TVPGQNV+A+KSG AQIADEKNGGYLVG	564
Sbjct	421	KEAASLRTNMILVGTDPLYGTMYNHSTGKPIITVPGQNVAVKSGAAQIADEKNGGYLVG	480
Query	565	LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ A	624
Sbjct	481	STNYIFSVVTMNPENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQSPA	540
Query	625	KALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGKTIKNSSAEEGKNLAPNQ K L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGKTIK +S EEG NLAPNQ	684
Sbjct	541	KNLDDKVTTESSYAMPSIKDISPGELAEALRRNLVQPIVVGTGKTIKETSVEEGTNLAPNQ	600
Query	685	QVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKI QVL+LSDK EE+PDYMGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI	744
Sbjct	601	QVLLLSDKVEEIPDMYGWKKETAETFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNIKKI	660
Query	745	TLTLGD 750 LTLGD	
Sbjct	661	KLTLGD 666	

>emb|CAA88919.1| penicillin-binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1149 bits (2971), Expect = 0.0, Method: Composition-based stats.
Identities = 592/666 (88%), Positives = 628/666 (94%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNGITYANMM+IKKELE AEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTE VSQ+T+DGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW	324
Sbjct	181	LSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITEDFVW	240
Query	325	RDILYQSNYEPGSTMKVMMMLAAAIIDNNTFPGGGEVFNSSSELKIADATIRDWDVNEGLTGGR	384
Sbjct	241	RDILYQSNYEPGS KVMMLA++IDNNTFP GE FNSSE KIADAT RDWDVNEGLT G	300
Query	385	MMTFSQGFHSSNVGMTLLLEQKMGDATWLDYLNRFKFGVPTFRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTFSQGFHSSNVGTSLLLEQKMGDATWLDYLNRFKFGVPTFRFGLTDEYAGQLPADNIVS	360
Query	445	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504
Sbjct	361	IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVS	420
Query	505	KDAASLRTNTMVLVGTDVPVYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGGYLVG	564
Sbjct	421	KEAASLRTNMILVGTDPLYGTMYNHYTGKPIITVPQGNVAVKSGTAQIADEKNGGYLVG	480
Query	565	LTDYIFSASVMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTA	624
Sbjct	481	T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ A	540
Query	625	KALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTGIKKNSSAEEGKNLAPNQ	684
Sbjct	541	K L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTGIK +S EEG NLAPNQ	600
Query	685	QVLILSDKAAEEVPDMYGWTKETAETLAKWLNIELEFGSGSTVQKQDVRANTAIKDIKKI	744
Sbjct	601	QVLLLSDKVEEIPDMYSWKKETAEFAKWLIELEFGSGSVVQKQDVRTNTAIKNIKKI	660
Query	745	TLTLGD 750	
Sbjct	661	LTLGD 666	

>emb|CAB65448.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=666

Score = 1148 bits (2970), Expect = 0.0, Method: Composition-based stats.
Identities = 594/666 (89%), Positives = 627/666 (94%), Gaps = 0/666 (0%)

Query	85	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	144
Sbjct	1	VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NLKQVSFGAKGNGITYANMMSIKKELE AEVKIGIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT	264
Sbjct	121	ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW	324
Sbjct	181	ISS LQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGIT+DFVW	240
Query	325	RDILYQSNYEPGSTMKVMMMLAAAIIDNNTFPGGGEVFNSSSELKIADATIRDWDVNEGLTGGR	384
Sbjct	241	RDILYQSNYEPGS MKVM LAAAIIDNNTFP GE FNSSE KIADAT RDWDVN GLT G	300
Query	385	MMTFSQGFHSSNVGMTLLLEQKMGDATWLDYLNRFKFGVPTFRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTFLQGFHSSNVGMSLLLEQKMGDATWLDYLNRFKFGVPTFRFGLTDEYAGQLPADNIVS	360
Query	445	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504

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Sbjct 361 IAQSSFGQGISVTQTQM+RA TAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVS 420
IAQSSFGQGISVTQTQMLRALTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVS

Query 505 KDAASLRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG 564
K+AAS TR +M+LVGTD+YGTMYNH TGKP +TVPGQNVA+KSGTAQIADEKNGGYLVG
Sbjct 421 KEAASLRTNMILVGTDPLYGTMYNHSTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVG 480

Query 565 LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLTQTTA 624
T+YIFS V+M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ A
Sbjct 481 STNYIFSVMTPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLTQSPA 540

Query 625 KALEQVSQQSPYPMPVSKDISPGDLAEELRRNLVQPIVVGTGTTIKNSSAEEGKNLAPNQ 684
K L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTTIK +S EEG NLAPNQ
Sbjct 541 KNLDKVTTESSYAMPSIKDISPGDLAEELRRNLVQPIVVGTGTTIKETSVEEGTNLAPNQ 600

Query 685 QVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGTVQKQDVRANTAIKDIKKI 744
QVL+LSDK EE+PMYGTWKETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI
Sbjct 601 QVLILSDKVEEIPMYGWWKETAETFAKWLIDIELEFEGSGSVVQKQDVRTNTAIKNIKKI 660

Query 745 TLTLGD 750
LTLGD
Sbjct 661 KLTLGD 666

```

>emb|CAA67012.1| penicillin-binding protein [Streptococcus pneumoniae]
Length=666

Score = 1148 bits (2970), Expect = 0.0, Method: Composition-based stats.
Identities = 590/666 (88%), Positives = 631/666 (94%), Gaps = 0/666 (0%)

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Query 85 VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP 144
VPIAEDATSYNVYAVID+ YKSATGKILYVE +QFNKVAEVFHKYLDME+E+YV+EQL+QP
Sbjct 1 VPIAEDATSYNVYAVIDKKYKSATGKILYVEDSQFNKVAEVFHKYLDMEAYVKEQLAQP 60

Query 145 NLKQVSFGAKNGITYANMMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH 204
NL QVSFGAK NGITYANMM+IKK+L+ A V+GIDFTTSPNRSYPNGQFASSFIGLAQLH
Sbjct 61 NLQVSFGAKENGITYANMMMAIKKDLKSDASVEGIDFTTSPNRSYPNGQFASSFIGLAQLH 120

Query 205 ENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDR LGNIVPGTEQVSQRTMDGKDVYTT 264
ENEDGSKSLLGT G+ESSLN+ILAGTDGIITYEKDR+GNIVPGTE VSQ+T+DGKDVYTT
Sbjct 121 ENEDGSKSLLGTGLESSLNTILAGTDGIITYEKDRVGNIVPGTELVSQQTVDGKDVYTT 180

Query 265 ISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITDFVW 324
+SSPLQSFMETQMDAF EKVKGYMTATLVSAKTGEILATTQRPTF+ADTK+GIT+DFVW
Sbjct 181 LSSPLQSFMETQMDAFLEKVKGYMTATLVSAKTGEILATTQRPTFNADTKDGITKDFVW 240

Query 325 RDILYQSNYEPGSTMKVMMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGR 384
RDILYQ NYEPGS MKVM LA++IDNNTFPGGE FNSSE KIAD T RDWDVNEGLTGGR
Sbjct 241 RDILYQGNYEPGSAMKVMMLASSIDNNTFPGGEYFNSSSEKIADVTTTRDWDVNEGLTGGG 300

Query 385 MMTFSQGFHSSNVGMILLQKMGDWTWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN 444
MMTFSQGFHSSNVGM LLE+KMGD TWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIV+
Sbjct 301 MMTFSQGFHSSNVGMILLQKMGDWTWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVS 360

Query 445 IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS 504
IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI+A+YDPNDQT RKSQKEIVGNPVS
Sbjct 361 IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFITALYDPNDQTVRKSQKEIVGNPVS 420

Query 505 KDAASLRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG 564
KDAAS TRT MVLVGTDVPVYGTMYNHSTGKP VTVPGQNVALKSGTAQIADEKNGGYLVG
Sbjct 421 KDAASQTRTQMVLVGTDVPVYGTMYNHSTGKPIVTVPGQNVALKSGTAQIADEKNGGYLVG 480

Query 565 LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLTQTTA 624
T+YIFS ++++PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SL LQ+ A
Sbjct 481 STNYIFSLLTINPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLYLQSPA 540

Query 625 KALEQVSQQSPYPMPVSKDISPGDLAEELRRNLVQPIVVGTGTTIKNSSAEEGKNLAPNQ 684
K L++V+ +S Y MPS+KDISPGDLAEELRRN+VQPIVVGTGTTIK SS EEG+NL+PNQ
Sbjct 541 KNLDKVTTESSYAMPSIKDISPGDLAEELRRNLVQPIVVGTGTTIKESSVEEGRNLSPNQ 600

Query 685 QVLILSDKAEVPMYGTWKETAETLAKWLNIELEFQSGSGTVQKQDVRANTAIKDIKKI 744
QVLILSDKAEVPMYGTWKETAET AKWLNIELEF+GSGSGTVQKQDVRANTAIKDIKKI
Sbjct 601 QVLILSDKAEVPMYGTWKETAETFAKWLNIIELEFEGSGSGTVQKQDVRANTAIKDIKKI 660

Query 745 TLTLGD 750
LTLGD
Sbjct 661 TLTLGD 666

```

>emb|CAA67010.1| penicillin-binding protein [Streptococcus pneumoniae]
Length=666

Score = 1146 bits (2964), Expect = 0.0, Method: Composition-based stats.
Identities = 586/666 (87%), Positives = 631/666 (94%), Gaps = 0/666 (0%)

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Query 85 VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP 144

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Sbjct	1	VPIAEDATSYNVYAVID+ YKSATGKILYVE +QFNKVAEVFHKYLDME+E+YV+EQL+QP VPIAEDATSYNVYAVIDKKYKSATGKILYVEDSQFNKVAEVFHKYLDMEAYVKEQLAQP	60
Query	145	NLKQVSFGAKGNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLAQLH	204
Sbjct	61	NL QVSFGAKGNGITYANMM+IKK+L+ A V+GIDFTTSPNRSYPNGQFASSFIGLAQLH NLTQVSFGAKGNGITYANMMAIKKDLK DASVEGIDFTTSPNRSYPNGQFASSFIGLAQLH	120
Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTT	264
Sbjct	121	ENEDGSKSLLGT G+ESSLN+ILAGTDGIIITYEKD +GNIVPGTE VSQ+T+DGKDVYTT ENEDGSKSLLGTGFGLESSLNTILAGTDGIIITYEKDGVGNIVPGTELVSSQQTVDGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVW	324
Sbjct	181	+SSPLQSFMETQMDAF +KVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVW LSSPLQSFMETQMDAFLQKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITEDFVW	240
Query	325	RDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGR	384
Sbjct	241	RDILYQ NYEPGS MKVM LA++IDNNTFPGGE FNSSE KIAD T RDWDVNEGLTGG RDILYQGNYEPGSAMKVMTLASSIDNNTFPGGEYFNSSSESKIADVTTTRDWDVNEGLTG	300
Query	385	MMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTFSQGFHSSNVGM LLE+KMGD TWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIV+ MMTFSQGFHSSNVGMILLEEKMGD TTWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVS	360
Query	445	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504
Sbjct	361	IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVG PVS IAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGKPV	420
Query	505	KDAASLRTNMLVVGTDVPYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVG	564
Sbjct	421	+DAASLRTNMLVVGTD+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG EDAASLRTNMLVVGTDPLYGTMYNHQTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVG	480
Query	565	LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGLGEFANPILERASAMKDSLNLQTTA	624
Sbjct	481	T+YIFS V+M+PAENPDFILYVTVQQPEH+SGIGLGEFANPILERASAMK+SLNLQ+ A STNYIFSVVTMNPENPDFILYVTVQQPEHFSIGLGEFANPILERASAMKESLNLQSPA	540
Query	625	KALEQVSQQSPYPMPVSKDISPGDLAEELRRNLVQPIVVGTTGKIKNSSAEEGKNLAPNQ	684
Sbjct	541	K L+QVS Q+ Y MPS+K+ISPGDLAEELRRN+VQPIVVGTTGKIK SS EEG+NL+PNQ KNLDQVSSQTSYAMPSIKNISPGDLAEELRRNIVQPIVVGTTGKIKESSVEEGRNLSPNQ	600
Query	685	QVLILSDKAAEVPDMYGWTKETAETLAKWLNIELEFGSGSTVQKQDVRANTAIKDIKKI	744
Sbjct	601	QVLILSDKAAEVPDMYGWTKETAET AKWLNIELEF+GSGSTVQKQDVRANTAIKDIKKI QVLILSDKAAEVPDMYGWTKETAETFAKWLNIELEFEGSGSTVQKQDVRANTAIKDIKKI	660
Query	745	TLTLGD 750	
Sbjct	661	+TLGD YITLGD 666	

>gb|AA56856.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=669

Score = 1145 bits (2961), Expect = 0.0, Method: Composition-based stats.
Identities = 587/669 (87%), Positives = 628/669 (93%), Gaps = 0/669 (0%)

Query	82	RNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL	141
Sbjct	1	RNGVPIAEDATSYNVYAVID+ YKSATGKILYVE QFNKVAEVFHKYLDME+E+YV+EQL RNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFNKVAEVFHKYLDMEAYVKEQL	60
Query	142	SQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKIDFTTSPNRSYPNGQFASSFIGLA	201
Sbjct	61	SQPNL QVSFGAKGNGITYANMM+IKKELE AEVKIDFTTSPNRSYPNGQFASSFIGLA SQPNLTQVSFGAKGNGITYANMMAIKKELETAEVKIDFTTSPNRSYPNGQFASSFIGLA	120
Query	202	QLHENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDV	261
Sbjct	121	QLHENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDRLGNIVPGTEQVSQ+T+DGKDV QLHENEDGSKSLLGTSGMESSLNSILAGKDGIIITYEKDRLGNIVPGTEQVSQQTVDGKDV	180
Query	262	YTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITED	321
Sbjct	181	YTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITED YTTLSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITED	240
Query	322	FVWRDILYQSNYEPGSTMKVMMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLT	381
Sbjct	241	FVWRDILYQSNYEPGS MKVM LA++IDNNTF GE FNSSE KIADAT RDWDVN+GLT FVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPGGEYFNSSSEFKIADATTRDWDVNDGLT	300
Query	382	GGRMMTFSQGFHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN	441
Sbjct	301	G MMTF QGFHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADN TGGMMTFLQGFHSSNVGMSLLEQKMGDATWLDYLKRFKFGVPTRFGLTDEYAGQLPADN	360
Query	442	IVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGN	501
Sbjct	361	IV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGN IVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGN	420
Query	502	PVSKDAASLRTNMLVVGTDVPYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGY	561
Sbjct	421	PVSK+AAS TR +M+LVGTD+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGY PVSKEAASLRTNMLVVGTDPLYGTMYNHYTGKPIITVPGQNVAVKSGTAQIADEKNGGY	480

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Query   562  LVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ  621
Sbjct   481  LVGSTNYIFSVVTMNPANPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQ  540

Query   622  TTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLA  681
Sbjct   541  SPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGTNLA  600

Query   682  PNQQVLILSDKAEVDPMYGWTKEAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDI  741
Sbjct   601  PNQQVLLSDKVEEIPDMYGWKKETAETFAKWLIDIELEFEGSGSVVQKQDVRTNTAIKNI  660

Query   742  KKITLTLGD 750
Sbjct   661  KKI LTLGD
        KKI LTLGD 669

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>gb|AAN32864.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

Score = 1143 bits (2956), Expect = 0.0, Method: Composition-based stats.
Identities = 588/661 (88%), Positives = 625/661 (94%), Gaps = 0/661 (0%)

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Query   90  DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV  149
Sbjct   1  DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV  60

Query   150  SFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG  209
Sbjct   61  SFGAKGNGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG  120

Query   210  SKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQRTMDGKDVYTTISSPL  269
Sbjct   121  SKSLLGTSGMESSLNSILAGTDGIIITYEKDRLGNIVPGTEQVSQ+T+DGKDVYTTISSPL  180

Query   270  QSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY  329
Sbjct   181  QSFMETQM+AFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEG+T+DFVWRDILY  240

Query   330  QSNYEPGSTMKVMMMLAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFS  389
Sbjct   241  QSNYEPGSAMKVMTLASSIDNNTFPSGEYFNSSEFKIADATTRDWDVNGGLTTGGMFTFL  300

Query   390  QGFAHSSNVGMTLLEQKMGGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS  449
Sbjct   301  QGFAHSSNVGM+LLEQKMGGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSS  360

Query   450  FGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKEAAS  509
Sbjct   361  FGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKEAAS  420

Query   510  LTRTNMVLVGTDVPYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNNGGYLVGLTDYI  569
Sbjct   421  TTRNHMILVGTDPLYGTYMYNHSTGKPIITVPGQNVAVKSGTAQIADEKNNGGYLVGSTNYI  480

Query   570  FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ  629
Sbjct   481  FSVVTMNPANPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQSPAKNLDK  540

Query   630  VSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQQVLIL  689
Sbjct   541  VTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGKNLAPNQQVLLL  600

Query   690  SDKAEVDPMYGWTKEAETLAKWLNIELEFQSGSGSTVQKQDVRANTAIKDIKKITLTLG  749
Sbjct   601  SDKVEEIPDMYGWKKETAETFAKWLIDIELEFEGSGSVVQKQDVRTNTAIKNIKKITLTLG  660

Query   750  D 750
Sbjct   661  D 661

```

>emb|CAA67011.1| penicillin-binding protein [Streptococcus pneumoniae]
Length=666

Score = 1141 bits (2952), Expect = 0.0, Method: Composition-based stats.
Identities = 583/666 (87%), Positives = 627/666 (94%), Gaps = 0/666 (0%)

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Query   85  VPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQP  144
Sbjct   1  VPIAEDATSYNVYAVID+YKSATGKILYVE+QFNKVAEVFHKYLDME+E+YV+EQL+QP  60

Query   145  NLKQVSFSGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLH  204
Sbjct   61  NLQVSFSGAKGNGITYANMM+IKK+L+ A+V+GIDFTT PNRSYNGQFASSFIGLAQLH  120

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Query	205	ENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDR LGNIVPGTEQVSQRTMDGKDVYTT	264
Sbjct	121	ENEDGSKSLLGT G+ESSLN+ILAGTDGIIITYEKDR+GNIVPGTE VSQ+T+DGKDVYTT	180
Query	265	ISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPFTDADTKEGITEDFVW	324
Sbjct	181	LSSPVQSFMETQMDAFLEKVKGYMTATLVSAKTGEILATTQRPFTFNADTKDGITKDFVW	240
Query	325	RDILYQSNYEPGSTMKVMM LAAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGR	384
Sbjct	241	RDILYQ NYEPGS MKVM LA++IDNNTFPGGE FNSSE KIAD TIRDWDVNEGLTGG	300
Query	385	MMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVN	444
Sbjct	301	MMTFSQGFAHSSNVG LLE+KMGD TWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIV+	360
Query	445	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS	504
Sbjct	361	IAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFI+A+YDPNDQT RKSQKEIVGNPVS	420
Query	505	KDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGGYLVG	564
Sbjct	421	KDAAS TRT MVLVGTDPVYGTMYNHSTGKP VTPVQGNVALKSGTAQIADEKNGGYLVG	480
Query	565	LTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQLGEFANPILERASAMKDSLNLQTTA	624
Sbjct	481	T+YIFS V+M+PAENPDFILYVTVQQPEH+SGIQLGEFANPILERASAMK+SLNLQ+ A	540
Query	625	KALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTTKIKNSSAEEGKNLAPNQ	684
Sbjct	541	K L+QV+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTTKIK +S EEGKNLAPNQ	600
Query	685	QVLILSDKAEVEPDMYGWTKETAETLAKWLNIELEFQSGSGSTVQKQDV RANTAIKDIKKI	744
Sbjct	601	QVL+LSDK EE+PDMYGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI	660
Query	745	TLTLGD 750	
Sbjct	661	LTLGD 666	

>gb|AA556840.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=667

Score = 1140 bits (2949), Expect = 0.0, Method: Composition-based stats.
Identities = 585/667 (87%), Positives = 626/667 (93%), Gaps = 0/667 (0%)

Query	84	GVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQ	143
Sbjct	1	GVPIAEDATSYNVYAVID+ YKSATGKILYE QFNKVAEVFHKYLD M+E+YV+EQLSQ	60
Query	144	PNLKQVSFGAKNGGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQL	203
Sbjct	61	PNL QVSFGAKNGGITYANMM+IKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQL	120
Query	204	HENEDGSKSLLGTSGMESSLNSILAGTDGIIITYEKDR LGNIVPGTEQVSQRTMDGKDVYTT	263
Sbjct	121	HENEDGSKSLLGTSGMESSLNSILAG DGIITYEKDR LGNIVPGTEQVSQ+T+DGKDVYTT	180
Query	264	TISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPFTDADTKEGITEDFV	323
Sbjct	181	T+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPFT+ADTKEGITEDFV	240
Query	324	WRDILYQSNYEPGSTMKVMM LAAAIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGG	383
Sbjct	241	WRDILYQSNYEPGS MKVM LA++IDNNTFPGGE FNSSE KIADAT RDWDVN+GLT G	300
Query	384	RMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIV	443
Sbjct	301	MMTF QGFAHSSNVGM+LLEQKMGDATWLDYL RKFVGVPTRFGLTDEYAGQLPADNIV	360
Query	444	NIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPV	503
Sbjct	361	+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPV	420
Query	504	SKDAASLRTNMVLVGTDPVYGTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGGYLV	563
Sbjct	421	SK+AS TR +M+LVGTD P+YGTMYNH TGKP +TVPGQNV A+KSGTAQIADEKNGGYLV	480
Query	564	GLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQLGEFANPILERASAMKDSLNLQTT	623
Sbjct	481	G T+YIFS V+M+PAENPDFILYVTVQQPEHYSIGIQLGEFA PILERASAMK+SLNLQ+	540
Query	624	AKALEQVSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTTKIKNSSAEEGKNLAPN	683
Sbjct	541	AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTGTTKIK +S EEG NLAPN	600

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Query   684   QQVLILSDKAEVPMYGWTKETAETLAKWLNIELEFQGGSGSTVQKQDVRANTAIKDIKK 743
Sbjct   601   QQVLLLSDKVEEIPDMYGWKKETAETFAKWLIDIELEFEGSGSVVQKQDVRTNTAIKNIKK 660

Query   744   ITLTLGD 750
          I LTLGD
Sbjct   661   IKLTLGD 667

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>gb|AAN32856.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=661

Score = 1139 bits (2945), Expect = 0.0, Method: Composition-based stats.
Identities = 586/661 (88%), Positives = 624/661 (94%), Gaps = 0/661 (0%)

```

Query   90    DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV 149
Sbjct   1     DATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQV 60

Query   150   SFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG 209
Sbjct   61    SFG+KNGITYANMMSIKKELE AEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDG 120

Query   210   SKSLLGTSGMESSLNSILAGTDGIITYEKDR LGNIVPGTEQVSQRTMDGKDVTYTTISSPL 269
Sbjct   121   SKSLLGTSGMESSLNSILAGTDGIITYEKDR+GNIVPGTE VSQ+T+DGKDVTYTT+SSPL 180

Query   270   QSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILY 329
Sbjct   181   QSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVWRDILY 240

Query   330   QSNYEPGSTMKVMMLAAAIIDNNTFPGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFS 389
Sbjct   241   QSNYEPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT G MMTF 300

Query   390   QGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSS 449
Sbjct   301   QGFAHSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSS 360

Query   450   FGQGISVTQTQMIRAFATAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAAS 509
Sbjct   361   FGQGISVTQTQMLRAFAATAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKEAAS 420

Query   510   LTRTNMVLVGTDPVYGYTMYNHSTGKPTVTVPQGNVALKSGTAQIADEKNGGYLVGLTDYI 569
Sbjct   421   TTRNHMILVGTDPVYGYTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG T+YI 480

Query   570   FSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQ 629
Sbjct   481   FSVVTMNPANPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQSPAKNLDK 540

Query   630   VSQQSPYPMPSPVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQVLLIL 689
Sbjct   541   VTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGTNLAPNQVLLL 600

Query   690   SDKAEVPMYGWTKETAETLAKWLNIELEFQGGSGSTVQKQDVRANTAIKDIKKITLTLG 749
Sbjct   601   SDK EE+PDYMGW KETAET AKWL+IELEF+GSGS VQKQDVR NTAIK+IKKI LTLG 660

Query   750   D 750
          D
Sbjct   661   D 661

```

>gb|ABB46508.1| penicillin binding protein 2x [Streptococcus pneumoniae]
Length=657

Score = 1135 bits (2936), Expect = 0.0, Method: Composition-based stats.
Identities = 583/657 (88%), Positives = 620/657 (94%), Gaps = 0/657 (0%)

```

Query   94    YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGA 153
Sbjct   1     YNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGA 60

Query   154   KNGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSL 213
Sbjct   61    KNGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSL 120

Query   214   LGTSGMESSLNSILAGTDGIITYEKDR LGNIVPGTEQVSQRTMDGKDVTYTTISSPLQSF 273
Sbjct   121   LGTSGMESSLNSILAGTDGIITYEKDR+GNIVPGTE VSQ+T+DGKDVTYTT+SSPLQSF 180

Query   274   ETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNY 333
Sbjct   181   ETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITEDFVWRDILYQSNY 240

```

```

Query   334   EPGSTMKVMMLAAAIIDNNTFPGGGEVFNSSSELKIADATIRDWDVNEGLTGGRMMTFSQGFA 393
Sbjct   241   EPGS MKVM LA++IDNNTFP GE FNSSE KIADAT RDWDVN+GLT G MMTF QGFA 300
          EPGSAMKVMTLASSIDNNTFPSGEYFNSSEFKIADATTRDWDVNDGLTTGGMMTFLQGFA

Query   394   HSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQG 453
Sbjct   301   HSSNVGM+LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADNIV+IAQSSFGQG 360
          HSSNVGMSLLEQKMGDATWLDYLKRFKFGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQG

Query   454   ISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVS KDAASLTRT 513
Sbjct   361   ISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGNPVS K+AAS TR 420
          ISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKEAASSTRN

Query   514   NMVLVGTDVPYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAV 573
Sbjct   421   HMILVGTDPLYGTMYNHYTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVGSTNYIFSVV 480
          +M+LVGTD+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGYLVG T+YIFS V

Query   574   SMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQTTAKALEQVSQQ 633
Sbjct   481   +M+PAENPDFILYVTVQQPEHYSGIQLGEFA PILERASAMK+SLNLQ+ AK L++V+ + 540
          TMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQSPAKNLDKVTTE

Query   634   SPYPMPSVKDISPGDLAEELRRNLVQPIVVGTTGKTIKNSAEKGKLNAPNQVVLISDKA 693
Sbjct   541   S Y MPS+KDISPG+LAE LRRN+VQPIVVGTTGTKIK +S EEG NLAPNQVVL+LSDK 600
          SSYAMPSIKDISPGELAEALRRNIVQPIVVGTTGTKIKETSVEEGTNLAPNQVVLISDKV

Query   694   EEVPDMYGWTKETATLAKWLNIELEFQSGSGSTVQKQDV RANTAIKDIKKITLTLGD 750
Sbjct   601   EE+PD MYGW KETAT AKWL+IELEF+GSGS VQKQDVR NTAIK+I KI LTLGD 657
          EEIPD MYGWKKETATFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNITKIKLTLGD

```

>gb|AA556855.1| penicillin-binding protein 2X [Streptococcus pneumoniae]
Length=669

Score = 1135 bits (2935), Expect = 0.0, Method: Composition-based stats.
Identities = 580/669 (86%), Positives = 626/669 (93%), Gaps = 0/669 (0%)

```

Query   82    RNVVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQL 141
Sbjct   1     RNVVPIAEDATSYNVYAVID+ YKSATGKILYVE QFNKVAEVFHKYLDME+YV+EQL 60
          RNVVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFNKVAEVFHKYLDMEAYVKEQL

Query   142   SQPNLKQVSFGAKNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLA 201
Sbjct   61    SQPNL QVSFGAKNGITYANMM+IKK+L+ A V+GIDFTTSPNRSYPNGQFASSFIGLA 120
          SQPNLTQVSFGAKNGITYANMMAIKKDLKADSAVEGIDFTTSPNRSYPNGQFASSFIGLA

Query   202   QLHENEDGSKSLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDV 261
Sbjct   121   QLHENEDGSKSLGTSG+ESSLN+ILAGTDGIITYEKDRLGNIVPGTEQVSQ+T+DGKDV 180
          QLHENEDGSKSLGTSGLESSLNTILAGTDGIITYEKDRLGNIVPGTEQVSQQTVDGKDV

Query   262   YTTISSPLQSFMETQMDAFQEKVKGYMTATLVSAKTGEILATTQRPTFDADTKEGITED 321
Sbjct   181   YTT+SSPLQSFMETQMDAF EKVKGKYMTATLVSAKTGEILATTQRPTF+ADTKEGITED 240
          YTTLSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITED

Query   322   FVWRDILYQSNEYEPGSTMKVMMLAAAIIDNNTFPGGGEVFNSSSELKIADATIRDWDVNEGLT 381
Sbjct   241   FVWRDILYQSNEYEPGS KVMMLA++IDNNTFP GE FNSSE KIADAT RDWDVN GLT 300
          FVWRDILYQSNEYEPGSAFKVMMLASSIDNNTFPSGEYFNSSEFKIADATTRDWDVNAGLT

Query   382   GGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADN 441
Sbjct   301   G MMTF QGFAHSSNVG +LLEQKMGDATWLDYL RFKFGVPTRFGLTDEYAGQLPADN 360
          TGGMMTFLQGFAHSSNVGTSLLLEQKMGDATWLDYLKRFKFGVPTRFGLTDEYAGQLPADN

Query   442   IVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGN 501
Sbjct   361   IV+IAQSSFGQGISVTQTQM+RAFTAIANDGVMLEPKFISAIYD N+Q+ RKSQKEIVGN 420
          IVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGN

Query   502   PVS KDAASLTRTNMVLVGTDVPYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGY 561
Sbjct   421   PVS K+AAS TR +M+LVGTD+YGTMYNH TGKP +TVPGQNV+KSGTAQIADEKNGGY 480
          PVSKEAASSTRNHMILVGTDPLYGTMYNHYTGKPIITVPGQNVAVKSGTAQIADEKNGGY

Query   562   LVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNLQ 621
Sbjct   481   LVG T+YIFS V+M+PAENPDFILYVTVQQPEH+SGIQLGEFA PILERASAMK+SLNLQ 540
          LVGSTNYIFSVVTMNPAENPDFILYVTVQQPEHFSGIQLGEFATPILERASAMKESLNLQ

Query   622   TTA KALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTTGKTIKNSAEKGKLNLA 681
Sbjct   541   + AK L++V+ +S Y MPS+KDISPG+LAE LRRN+VQPIVVGTTGTKIK +S EEG NLA 600
          SPAKNLDKVTTESSYAMPSIKDISPGELAEALRRNIVQPIVVGTTGTKIKETSVEEGTNLA

Query   682   PNQQVVLISDKAEVDPD MYGWTKETATLAKWLNIELEFQSGSGSTVQKQDV RANTAIKDI 741
Sbjct   601   PNQQVVL+LSDK EE+PD MYGW KETAT AKWL+IELEF+GSGS VQKQDVR NTAIK+I 660
          PNQQVVLISDKVEEIPD MYGWKKETATFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNI

Query   742   KKITLTLGD 750
Sbjct   661   KKI LTLGD 669
          KKI LTLGD
          KKIKLTLGD

```

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Posted date: May 31, 2007 5:55 PM
Number of letters in database: 146,036
Number of sequences in database: 262

Lambda	K	H
0.313	0.130	0.362

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 262
Number of Hits to DB: 1868
Number of extensions: 66
Number of successful extensions: 3
Number of sequences better than 10: 1
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 750
Length of database: 146036
Length adjustment: 77
Effective length of query: 673
Effective length of database: 125862
Effective search space: 84705126
Effective search space used: 84705126
T: 11
A: 40
X1: 16 (7.2 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 42 (20.8 bits)
S2: 48 (23.1 bits)